

Genome version 4.5
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OM protein - protein search, using SW model

Run on: April 11, 2002, 09:52:49 : Search time 12.57 seconds

(without alignments)
472,710 Million cell updates/sec

Hit(s): US-09-609-543-2

Perfect score: 1118

Sequence: 1 MAP1A/US09-609-543-2.....PROTEINUS09-609-543-2

Scoring table:

Gapop 10.0, Gapext 0.5

Seal: 212252 2000 2000 2000 2000

Minimum hit seq length: 0

Maximum hit seq length: 2000000000

Post processing: Minimum Match 0%

Database: Issued Patent: AA*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match	Length	DB	ID	Description
1	774.5	69.3	208	1	US-08-340-820-8	Sequence 2, April
2	774.5	69.3	208	1	US-08-340-820-9	Sequence 9, April
3	774.5	69.3	208	1	US-08-340-820-10	Sequence 10, April
4	774.5	69.3	208	1	US-08-340-820-11	Sequence 11, April
5	774.5	69.3	208	1	US-08-340-820-12	Sequence 12, April
6	774.5	69.3	208	1	US-08-340-820-13	Sequence 13, April
7	774.5	69.3	208	1	US-08-340-820-14	Sequence 14, April
8	774.5	69.3	208	1	US-08-340-820-15	Sequence 15, April
9	774.5	69.3	208	1	US-08-340-820-16	Sequence 16, April
10	774.5	69.3	208	1	US-08-340-820-17	Sequence 17, April
11	774.5	69.3	208	1	US-08-340-820-18	Sequence 18, April
12	774.5	69.3	208	1	US-08-340-820-19	Sequence 19, April
13	774.5	69.3	208	1	US-08-340-820-20	Sequence 20, April
14	774.5	69.3	208	1	US-08-340-820-21	Sequence 21, April
15	774.5	69.3	208	1	US-08-340-820-22	Sequence 22, April
16	774.5	69.3	208	1	US-08-340-820-23	Sequence 23, April
17	774.5	69.3	208	1	US-08-340-820-24	Sequence 24, April
18	774.5	69.3	208	1	US-08-340-820-25	Sequence 25, April
19	774.5	69.3	208	1	US-08-340-820-26	Sequence 26, April
20	774.5	69.3	208	1	US-08-340-820-27	Sequence 27, April
21	774.5	69.3	208	1	US-08-340-820-28	Sequence 28, April
22	774.5	69.3	208	1	US-08-340-820-29	Sequence 29, April
23	774.5	69.3	208	1	US-08-340-820-30	Sequence 30, April
24	774.5	69.3	208	1	US-08-340-820-31	Sequence 31, April
25	774.5	69.3	208	1	US-08-340-820-32	Sequence 32, April
26	774.5	69.3	208	1	US-08-340-820-33	Sequence 33, April
27	774.5	69.3	208	1	US-08-340-820-34	Sequence 34, April

28	758.5	67.8	206	1	US-08-340-820-8	Sequence 8, April
29	758.5	67.8	206	1	US-08-172-828-5	Sequence 5, April
30	758.5	67.8	206	1	US-08-593-535-7	Sequence 7, April
31	758.5	67.8	206	1	US-08-593-535-8	Sequence 8, April
32	742	66.4	175	1	US-08-172-828-6	Sequence 6, April
33	742	66.4	175	1	US-08-172-828-7	Sequence 7, April
34	742	66.4	175	1	US-08-440-820-4	Sequence 4, April
35	742	66.4	175	1	US-08-593-535-4	Sequence 4, April
36	742	66.4	175	1	US-08-840-820-4	Sequence 4, April
37	742	66.4	175	1	US-08-593-535-5	Sequence 5, April
38	729	65.2	159	1	US-08-172-828-8	Sequence 8, April
39	729	65.2	159	1	US-08-172-828-9	Sequence 9, April
40	718.5	64.6	133	2	US-08-440-820-21	Sequence 21, April
41	718.5	64.6	133	2	US-08-593-535-7	Sequence 7, April
42	705.5	63.1	207	2	US-08-943-915-2	Sequence 2, April
43	702.5	62.8	190	1	US-08-441-629-16	Sequence 16, April
44	702.5	62.8	190	6	US-08-776-267-16	Sequence 16, April
45	702.5	62.8	190	6	PT-0895-09172-16	Sequence 16, April
46	691.5	61.9	139	2	US-08-943-915-1	Sequence 1, April
47	688	61.1	142	1	US-08-840-820-1	Sequence 1, April
48	688	61.1	142	1	US-08-172-828-1	Sequence 1, April
49	688	61.1	142	1	US-08-593-535-1	Sequence 1, April
50	676	59.9	173	2	US-08-943-915-12	Sequence 12, April

ALIGNMENTS

RESULT 1

US-08-340-820-3

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US-08-340-820-3

CLONE: PGAR1
US-08-593-543-25

Query Match: 69.38; Score: 774.5; DB: 1; Length: 208;
Host Local Similarity: 70.68; Pred. No. 1.9e-79;
Matches: 149; Conservative: 24; Mismatches: 80; Gaps: 9; Cuts: 4;

QY 1 MAPIAVGDTLGLGNTLMDVNSHFLTPAGRPPLTGERPSAENSARQ--GTSAAAL 57
DB 1 MAPIAVGDTLGLGNTLMDVNSHFLTPAGRPPLTGERPSAENSARQ--GTSAAAL 57
QY 58 AHHGHTLRRLVYCRVGRVHQLDQSVQVQTRQSHSTPTDRTSVAVGVSTRVDSGL 117
DB 55 DILKLLRRLVYCRVGRVHQLDQSVQVQTRQSHSTPTDRTSVAVGVSTRVDSGL 114
QY 118 YLHGGHTLRRLVYCRVGRVHQLDQSVQVQTRQSHSTPTDRTSVAVGVSTRVDSGL 117
DB 115 YLHGGHTLRRLVYCRVGRVHQLDQSVQVQTRQSHSTPTDRTSVAVGVSTRVDSGL 114
QY 178 GABSGHGGGTHHLPVGVGVVGVVGL 209
DB 175 GRTVGGGTHHLPVGVGVVGVVGL 205

RESULT 8

US-08-439-725A-7
Sequence 7; Application US/08419725A
Patent No. 5643775
GENERAL INFORMATION:
APPLICANT: Nathans, Jeremy
APPLICANT: Smallwood, Philip M.
APPLICANT: Macko, Jennifer P.
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR PROMOTORS
TITLE OF INVENTION: FACTOR 1 (Fgf-1) AND METHODS OF USE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 425 Executive Square, Suite 1400
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90047
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC/XT/AT/PS/2
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent to Release #10; Version #1.10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,725A
FILING DATE: 12 MAY 1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baile, Lisa A.
REGISTRATION NUMBER: 48,147
REFERENCE/EXCIT NUMBER: 7255,947,001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-439-725A-7

Query Match: 69.38; Score: 774.5; DB: 1; Length: 208;
Host Local Similarity: 70.68; Pred. No. 1.9e-79;
Matches: 149; Conservative: 24; Mismatches: 80; Gaps: 9; Cuts: 4;

QY 1 MAPIAVGDTLGLGNTLMDVNSHFLTPAGRPPLTGERPSAENSARQ--GTSAAAL 57
DB 1 MAPIAVGDTLGLGNTLMDVNSHFLTPAGRPPLTGERPSAENSARQ--GTSAAAL 57
QY 58 AHHGHTLRRLVYCRVGRVHQLDQSVQVQTRQSHSTPTDRTSVAVGVSTRVDSGL 117
DB 55 DILKLLRRLVYCRVGRVHQLDQSVQVQTRQSHSTPTDRTSVAVGVSTRVDSGL 114
QY 118 YLHGGHTLRRLVYCRVGRVHQLDQSVQVQTRQSHSTPTDRTSVAVGVSTRVDSGL 117
DB 115 YLHGGHTLRRLVYCRVGRVHQLDQSVQVQTRQSHSTPTDRTSVAVGVSTRVDSGL 114
QY 178 GABSGHGGGTHHLPVGVGVVGVVGL 209
DB 175 GRTVGGGTHHLPVGVGVVGVVGL 205

RESULT 9

US-08-462-169B-17
Sequence 17; Application US/08462169B
Patent No. 577252
GENERAL INFORMATION:
APPLICANT: John Greene and Craig A. Rosen
TITLE OF INVENTION: Fibroblast Growth Factor-15
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELIA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CROCHET, STEWART & OLSTEIN
STREET: 6 BUCKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
FILING DATE: 05 JUN 95
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MILLINS, J.C.
REGISTRATION NUMBER: 45,074
REFERENCE/EXCIT NUMBER: 45,074
FILING DATE: 05 JUN 1995
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-462-169B-17

Query Match: 69.38; Score: 774.5; DB: 1; Length: 208;
Host Local Similarity: 70.68; Pred. No. 1.9e-79;
Matches: 149; Conservative: 24; Mismatches: 80; Gaps: 9; Cuts: 4;

QY 1 MAPIAVGDTLGLGNTLMDVNSHFLTPAGRPPLTGERPSAENSARQ--GTSAAAL 57
DB 1 MAPIAVGDTLGLGNTLMDVNSHFLTPAGRPPLTGERPSAENSARQ--GTSAAAL 57
QY 58 AHHGHTLRRLVYCRVGRVHQLDQSVQVQTRQSHSTPTDRTSVAVGVSTRVDSGL 117
DB 55 DILKLLRRLVYCRVGRVHQLDQSVQVQTRQSHSTPTDRTSVAVGVSTRVDSGL 114
QY 118 YLHGGHTLRRLVYCRVGRVHQLDQSVQVQTRQSHSTPTDRTSVAVGVSTRVDSGL 117
DB 115 YLHGGHTLRRLVYCRVGRVHQLDQSVQVQTRQSHSTPTDRTSVAVGVSTRVDSGL 114

APPELLANT: SEKOU, Satchiko

[illegible]

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1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/08/340,820
3 FILING DATE:
4 CLASSIFICATION: 435
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: 02-07,835,714
7 FILING DATE:
8 ATTORNEY/AGENT INFORMATION:
9 NAME: GEBLIP, David G.
10 REGISTRATION NUMBER: 27026
11 TELECOMMUNICATION INFORMATION:
12 TELEPHONE: (617) 523-3400
13 TELEFAX: (617) 524-6440
14 TELEX: 200291 STPE OR
15 INTERNATIONAL CLASSIFICATION NO: 5:
16 SEQUENCE CHARACTERISTICS:
17 LENGTH: 205 amino acids
18 TYPE: amino acid
19 TOPOLOGY: linear
20 MOLECULE TYPE: protein
21 US 08-340-R20-5

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Query Match	67.8%	Score 758.5	DB 1	Length 2052	
Host Local Similarity	70.28%	Prod. No. 1-20	772		
Matches 1462	Conserved 283	Matches 402	Indels 9	Gaps	
Q7	4	LAEEVPEPLGELRLGAGQVSHPELLPPACSEKRPGLAERSAAERSAAGC--GPAAGALAIL	60		
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Db	1	LAEEVNPVGVQVAV--PPEVNPVLYV--DSPVLSIDHLDGSE--AGLPGAVVIMIDH	64		
Q7	61	HEELERKQLYCRVGRPHGLPLPSVSGCTQQHDSLEPLLEFLISAVALLVSLPVLSGLYD	120		
	1	1 1			
Db	55	KALLERKQLYCRVGRPHGLPLPNCGLVGGTRKHDSKPELLEFLISAVALLVSLPVLSGLYD	114		
Q7	121	HEHKKRQVYSEKRLVSLGSELEELTPEKRYEYSLNLYEKREELDEKRVAVLNPDELLPEKQAK	180		
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Db	115	HEHKKRQVYSEKRLVSLGSELEELTPEKRYEYSLNLYEKREELDEKRVAVLNPDELLPEKQAK	174		
Q7	141	SKRHQETLPELPVWPEKRVPELYKILL	208		
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Db	175	SKRHQETLPELPVWPEKRVPELYKILL	202		

1 RESUBMIT 25
 2 US 08-172-328-4
 3 Sequence # 4 Application 05/08/172-328
 4 Patent No. 5571895
 5
 6 GENERAL INFORMATION:
 7 APPLICANT: KUROKAWA, Tsutomu
 8 APPLICANT: KUROKAWA, Ken-ichi
 9 APPLICANT: YOSHITOMI, Sumio
 10 APPLICANT: SERO, Sachiko
 11 TITLE OF INVENTION: ANTIBODIES, POLYPEPTIDES, PRODUCTION AND
 12 TITLE OF INVENTION: USE THEREOF
 13 NUMBER OF SEQUENCES: 12
 14
 15 CORRESPONDENT ADDRESS:
 16 ADDRESSEE: DAVITO G. COALIN, LINC. BROOKFIELD, RHODE IS.
 17 ADDRESSEE: CUSHMAN
 18 STREET: 140 Water Street
 19 CITY: Boston
 20 STATE: Massachusetts
 21 COUNTRY: US
 22 ZIP: 02109
 23
 24 COMPUTER READABLE FORM:
 25 MEDIUM TYPE: Floppy disk
 26 COMPUTER: IBM pc compat file
 27 OPERATING SYSTEM: PC DOS/MS-DOS
 28 SOFTWARE: Patent In Release #1.0, Version #1.25
 29 CURRENT APPLICATION DATA:
 30 APPLICATION NUMBER: 05/08/172-328
 31 FILING DATE:
 32 CLASSIFICATION: 435

NAME: 'NININ', 'NININ', 'NININ'

100

MOLECULAR TYPE: protein
HYDROPHOBICITY: NO

MOLECULE TYPE: Protein

MOLECULE TYPE: Protein


```

1 APPLICANT: Smallwood, Phillip M.
2
3 APPLICANT: Moskoy, Jennifer P.
4
5 TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR PROMOTORS
6
7 TITLE OF INVENTOR: FANTON, J. AND METHODS OF USE
8
9 NUMBER OF SEQUENCES: 25
10
11 CORRESPONDENT: Agence
12
13 ADDRESSEE: Fish & Richardson P.C.
14
15 STREET: 4225 Brown Tree Square, Suite 1400
16
17 CITY: Los Angeles
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19 STATE: CA
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21 COUNTRY: USA
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23 ZIP: 90047
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25 COMPUTER READABLE FORM:
26
27 MEDIUM TYPE: Floppy disk
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29 COMPUTER: IBM pc compatible
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31 OPERATING SYSTEM: PC DOS/MS DOS
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33 SOFTWARE: Patent in Release #1.0, Version #1.40
34
35 CURRENT APPLICATION DATA:
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37 APPLICANT'S SERIAL: 09/094915
38
39 FILING DATE: May 12, 1995
40
41 CLASSIFICATION: 435
42
43 ALTERNATIVE/AGENT INFORMATION:
44
45 NAME: Heller, Lisa A.
46
47 REGISTRATION NUMBER: 48,847
48
49 REFERENCE/WORKS CITED: 2044041
50
51 TELEPHONE: 619/678 5070
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53 TELEFAX: 619/678 5099
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55 INFORMATION FOR SERIAL NO.: 212
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57 SOURCE CHARACTERISTICS:
58
59 LENGTH: 193 amino acids
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61 TYPE: amino acid
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63 STRANDNESS: not relevant
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65 TOPLOGY: linear
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67 MOLECULE TYPE: protein
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APPLICATION NUMBER: 92/5741, 51
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: MIZEL, RICHARD J.
 REGISTRATION NUMBER: 27,657
 REFERENCE/LOCAL NUMBER: A-469
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 805,447,4112
 TELEFAX: 805,447,1040
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 207 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PS-ORF-YES/NO: 1/0

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1 RESULT 4
 2 US-08-441-629-16
 3 Sequence 16, April 17, 1994 08:00:44:16Z
 4 Patent No. 5766924
 5
 6 ORIGINAL INFORMATION
 7
 8 APPLICANT: Kirschner, Marc W.
 9 APPLICANT: Kirschner, Marc W.
 10 TITLE OF INVENTION: REPERFORATED ANVAY
 11 NUMBER OF SEQUENCE: 17
 12 CURRENT INVENTOR ADDRESS
 13 ADDRESS: 12411 G. Street, Belmont, MA 02458
 14 STREET: Two Mill Drive
 15 CITY: Lexington
 16 STATE: Massachusetts
 17 COUNTRY: USA
 18 ZIP: 02173
 19
 20 COMPUTER READABLE FORM
 21 MEDIUM TYPE: floppy disk
 22 COMPILER: IBM PC compatible
 23 OPERATING SYSTEM: PC DOS/MS DOS
 24 SOFTWARE: Patent in Release #1.0, Version #1.30
 25
 26 CURRENT APPLICATION DATA
 27 APPLICATION NUMBER: US/95/441,629
 28 FILING DATE: 15-MAY 1995
 29 CLASSIFICATION: A45
 30 PREVIOUS APPLICATION DATA:
 31 APPLICATION NUMBER: US 08/279,217
 32 FILING DATE: 22-MAY-1994
 33 AUTHORITY/NOTE INFORMATION:
 34 NAME: Granahan, Patricia
 35 REGISTRATION NUMBER: 32,227
 36 REFERENCE TO OTHER INFO: 15

TITLE: PHENYLALANINE DEGRADATION
 TELEPHONE: (611) 861-6240
 ADDRESS: (617) 861-9740
 INFORMATION: 106 SEC 10 NOV 1967
 SUBJECT: PHENYLALANINE
 LENGTH: 190 amino acids
 TYPE: amino acid
 STANDARDS: single
 PURITY: linear
 MOLECULE TYPE: protein
 OS-OR-441 629-16

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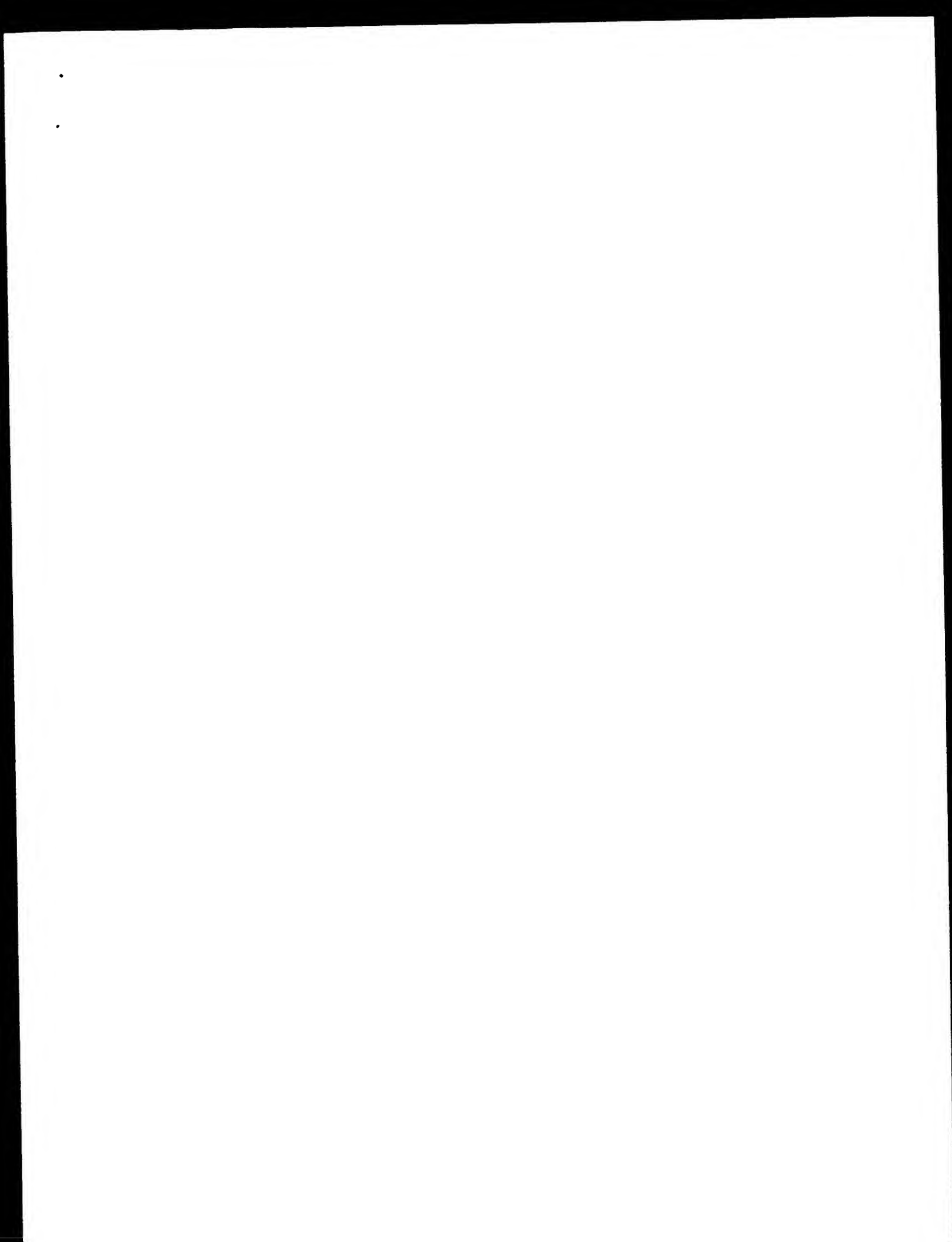
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01 RESULT 44
02 US-08-776-207-16
03 -----
04 PATENT NO. 6080718
05 GENERAL INFORMATION:
06 APPLICANT: Kirschner, Marc W.
07 TITLE OF INVENTION: Recipient Directed Assay
08 FILE REFERENCE: 0095 01A2
09 -----
10 CHERKIN FILING DATE: 1992-06-24
11 EARLIER APPLICATION NUMBER: 09/077,793/172
12 EARLIER FILING DATE: 1995-07-19
13 EARLIER ATTORNEY: R. M. BRESLER, 19-441, 6-29
14 EARLIER FILING DATE: 1995-04-15
15 EARLIER APPLICATION NUMBER: 09/279,217
16 EARLIER FILING DATE: 1994-07-22
17 PRIORITY CLAIM TO:
18 SOFTWARE: FASTSEQ for Windows Version 4.0
19 SEQ ID NO: 16
20 LENGTH: 190
21 TYPE: prt
22 ORGANISM: Homo sapiens
23 US-08-776-207-16

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31	1	1	1	1	1	1
32	1	1	1	1	1	1
33	1	1	1	1	1	1
34	1	1	1	1	1	1
35	1	1	1	1	1	1
36	1	1	1	1	1	1
37	1	1	1	1	1	1
38	1	1	1	1	1	1
39	1	1	1	1	1	1
40	1	1	1	1	1	1
41	1	1	1	1	1	1
42	1	1	1	1	1	1
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46	1	1	1	1	1	1
47	1	1	1	1	1	1
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49	1	1	1	1	1	1
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57	1	1	1	1	1	1
58	1	1	1	1	1	1
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63	1	1	1	1	1	1
64	1	1	1	1	1	1
65	1	1	1	1	1	1
66	1	1	1	1	1	1
67	1	1	1	1	1	1
68	1	1	1	1	1	1
69	1	1	1	1	1	1
70	1	1	1	1	1	1
71	1	1	1	1	1	1
72	1	1	1	1	1	1
73	1	1	1	1	1	1
74	1	1	1			

[illegible]



GenInfo version 4.5
Copyright (c) 1997-2000 Empower, Ltd.

0M protein - protein search, using SW model

Run on: April 11, 2002, 09:52:49 : Search time 24.25 seconds

(without alignments)
672,245 Million cell database

Title: us-09-609-543-2

Perfect score: 1118

Sequence: 1 MALVAVGCHTALLENHSDG.....PRVVEPVETKILMYI 211

Scoring table:

BLAST/MS62
Gapop 10.0, Gapext 9.5

Search: 522463 seqs, 74074290 residues

Minimum number of hits satisfying chosen parameters: 522463

Minimum hit seq length: 9

Maximum hit seq length: 200000000

Post-processing: Minimum Match 1008
Listing first 50 summaries

Database:

A_Genoseq_1101.*

- 1: 774.5 69.3 208 19 AAW75719
- 2: 774.5 69.3 208 19 AAW5424
- 3: 774.5 69.3 208 21 AAW15299
- 4: 774.5 69.3 208 21 AAW87856
- 5: 774.5 69.3 208 21 AAW90418
- 6: 774.5 69.3 208 21 AAW54341
- 7: 774.5 69.3 208 22 AAW60410
- 8: 774.5 69.3 208 22 AAW61663
- 9: 774.5 69.3 208 22 AAW50295
- 10: 774.5 69.3 208 22 AAW50719
- 11: 774.5 69.3 208 22 AAW50719
- 12: 774.5 69.3 208 22 AAW50719
- 13: 774.5 69.3 208 22 AAW50719
- 14: 774.5 69.3 208 22 AAW50719
- 15: 774.5 69.3 208 22 AAW50719
- 16: 774.5 69.3 208 22 AAW50719
- 17: 774.5 69.3 208 22 AAW50719
- 18: 774.5 69.3 208 22 AAW50719
- 19: 774.5 69.3 208 22 AAW50719
- 20: 774.5 69.3 208 22 AAW50719
- 21: 774.5 69.3 208 22 AAW50719
- 22: 774.5 69.3 208 22 AAW50719

prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	Hit	Insertion
1	1118	100.0	211	21	AAW18635
2	1118	100.0	211	22	AAW02981
3	1118	100.0	211	22	AAW62817
4	1074	96.1	212	22	AAW02090
5	774.5	69.3	220	18	AAW11548
6	774.5	69.3	208	14	AAW7207
7	774.5	69.3	208	13	AAW27212
8	774.5	69.3	208	15	AAW56505
9	774.5	69.3	208	16	AAW80784
10	774.5	69.3	208	16	AAW70822
11	774.5	69.3	208	18	AAW11547

12	774.5	69.3	208	19	AAW75719	Fibroblast growth factor (FGF)-20
13	774.5	69.3	208	19	AAW5424	Fibroblast growth factor (FGF)-20
14	774.5	69.3	208	21	AAW15299	Fibroblast growth factor (FGF)-20
15	774.5	69.3	208	21	AAW87856	Fibroblast growth factor (FGF)-20
16	774.5	69.3	208	21	AAW90418	Fibroblast growth factor (FGF)-20
17	774.5	69.3	208	21	AAW54341	Fibroblast growth factor (FGF)-20
18	774.5	69.3	208	22	AAW60410	Fibroblast growth factor (FGF)-20
19	774.5	69.3	208	22	AAW61663	Fibroblast growth factor (FGF)-20
20	774.5	69.3	208	22	AAW50295	Fibroblast growth factor (FGF)-20
21	774.5	69.3	208	22	AAW50719	Fibroblast growth factor (FGF)-20
22	774.5	69.3	208	22	AAW50719	Fibroblast growth factor (FGF)-20
23	774.5	69.3	208	22	AAW50719	Fibroblast growth factor (FGF)-20
24	774.5	69.3	208	22	AAW50719	Fibroblast growth factor (FGF)-20
25	774.5	69.3	208	22	AAW50719	Fibroblast growth factor (FGF)-20
26	774.5	69.3	208	22	AAW50719	Fibroblast growth factor (FGF)-20
27	774.5	69.3	208	22	AAW50719	Fibroblast growth factor (FGF)-20
28	774.5	69.3	208	22	AAW50719	Fibroblast growth factor (FGF)-20
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30	774.5	69.3	208	22	AAW50719	Fibroblast growth factor (FGF)-20
31	774.5	69.3	208	22	AAW50719	Fibroblast growth factor (FGF)-20
32	774.5	69.3	208	22	AAW50719	Fibroblast growth factor (FGF)-20
33	774.5	69.3	208	22	AAW50719	Fibroblast growth factor (FGF)-20
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35	774.5	69.3	208	22	AAW50719	Fibroblast growth factor (FGF)-20
36	774.5	69.3	208	22	AAW50719	Fibroblast growth factor (FGF)-20
37	774.5	69.3	208	22	AAW50719	Fibroblast growth factor (FGF)-20
38	774.5	69.3	208	22	AAW50719	Fibroblast growth factor (FGF)-20
39	774.5	69.3	208	22	AAW50719	Fibroblast growth factor (FGF)-20
40	774.5	69.3	208	22	AAW50719	Fibroblast growth factor (FGF)-20
41	774.5	69.3	208	22	AAW50719	Fibroblast growth factor (FGF)-20
42	774.5	69.3	208	22	AAW50719	Fibroblast growth factor (FGF)-20
43	774.5	69.3	208	22	AAW50719	Fibroblast growth factor (FGF)-20
44	774.5	69.3	208	22	AAW50719	Fibroblast growth factor (FGF)-20
45	774.5	69.3	208	22	AAW50719	Fibroblast growth factor (FGF)-20
46	774.5	69.3	208	22	AAW50719	Fibroblast growth factor (FGF)-20
47	774.5	69.3	208	22	AAW50719	Fibroblast growth factor (FGF)-20
48	774.5	69.3	208	22	AAW50719	Fibroblast growth factor (FGF)-20
49	774.5	69.3	208	22	AAW50719	Fibroblast growth factor (FGF)-20
50	774.5	69.3	208	22	AAW50719	Fibroblast growth factor (FGF)-20

RESIDUE 1 4
 ID AAB62817 STANDARD, PROTEIN, 211 AA.
 AA AAB62817
 XX
 02-MAY-2001 (first entry)
 DE Human fibroblast growth factor- α (FGF- α) amino acid sequence
 XX
 KW Fibroblast growth factor- α (FGF- α) useful in treating bone metastases;
 KW cell growth; proliferation; tumour; osteonosis; psoriasis; human;
 KW doppler's syndrome; kapost sarcoma; rheumatoid arthritis;
 KW cartilage repair; bone repair; exsiccation; healing; valvular deformity;
 KW atherosclerosis; cerebral ischaemia; cerebral ischaemia; stroke;
 KW Alzheimer's disease; diabetic neuropathy; osteoporosis.
 XX
 OS Homo sapiens.
 XX
 W0200107555-A2.
 XX
 ID 01-FEB-2001.
 XX
 27-JUL-2000; 2000WO-0820405.
 XX
 27-JUL-1999; 9408-0145899.
 XX 31 JAN 2000; 2000DS-0345895.
 XX 03-JUL-2000; 2000DS-0609543.
 XX
 (China) CHINA:CN 999P
 XX
 Jellies M, Shimkels KA, Prayaga SK, Kolding PL, Yang M, Burgess CJ,
 P1 Fernandes E, Herrmann JL, Larochole WJ, Lichenstein H,
 XX WPI: 2001-159717/16
 DE N-PSDB: AAF62049.
 XX
 New human fibroblast growth factor FGF- α polypeptide, useful for
 P1 treating tissue proliferation disorders such as tumors, osteonosis,
 P1 psoriasis, diabetic complications, Kapost sarcoma and rheumatoid
 P1 arthritis -
 XX
 PS Claim 1: Flg 1: 128pp; English.
 XX
 This invention relates to human fibroblast growth factor- α (FGF- α) and
 CC the DNA sequence encoding it. FGF- α protein and polypeptide sequences
 CC are useful for treating or preventing a disorder associated with aberrant
 CC expression, processing or physiological interactions of FGF- α .
 CC Characterized by identification of the amino acid sequence of a full-length
 CC FGF- α is also useful for promoting growth of cells which are in the
 CC vicinity of a wound, vascular system, those involved in hematopoiesis or
 CC erythropoiesis, cells in the lining of the gastrointestinal tract or
 CC cells in hair follicles. Other uses include: inhibiting cell growth,
 CC FGF- α is useful for treating, preventing or delaying a tissue
 CC proliferative disorder such as tumors, osteonosis, psoriasis,
 CC doppler's syndrome, kapost sarcoma, rheumatoid arthritis, and
 CC rheumatoid arthritis. Compositions containing FGF- α can be used to
 CC stimulate cartilage or bone repair. Compositions containing FGF- α
 CC binding agents can be used to treat diseases such as multiple or solitary
 CC hereditary osteonosis, valvular disease, deformity and atherosclerosis. FGF- α
 CC may be used in diagnosing or treating distal cell related disorders,
 CC cerebral lesions or to treat cerebral edema, senile dementia,
 CC Alzheimer's disease, or diabetic neuropathy. FGF- α also has
 CC osteonosis-promoting activity and can be used for treating bone
 CC fractures and osteoporosis. FGF- α polypeptides may be used as fibrinolytic
 CC increasing agents, or for treating cerebral nervous diseases. The present
 CC sequence represents the human FGF- α protein.
 XX
 Sequence 211 AA

query Match: 100.0%; Score 118; DB 22; Length 2115

[illegible]

C	AAM75-196
XX	07 Dec 1998 (first entry)
UI	
XX	Fibroblast growth factor-9.
EE	
XX	Fibroblast growth factor-9; FGF-9; mitogenic protein engineering;
KW	hepatitis B virus; thrombasthenia; thrombocytopenic; opthalmic disorder?
KM	hemorrhagic diathesis.
KX	
XX	Homo sapiens:
OS	
XX	Key:
EH	Misc difference 146
ET	/note
FT	"Phe-146 is replaced by another amino acid
FI	acid (claim 1), preferably Ala, Phe, Ser,
FE	Gly, Met, Leu or Tyr, especially Ala, Gly
FF	or Ser"
FI	Misc difference 147
FT	/note
FE	"Glu-147 may be replaced by another amino
FI	acid (claim 7), preferably Ala, Gly or Ser"
FE	Misc difference 148
FI	/note
FE	"Asn-148 may be replaced by another amino
FI	acid (claim 1), preferably Ala, Phe, Ser,
FE	Gly, Met, Leu or Tyr, especially Ala, Gly
FI	or Ser"
FI	Misc difference 149
FE	/note
FI	"Asn-149 may be replaced by another amino
FE	acid (claim 1), preferably Ala, Phe, Ser,
FI	Gly, Met, Leu or Tyr, especially Ala, Gly
FI	or Ser"
FN	WO9839436, A2.
XX	
XX	II Sep 1998.
XU	
XX	03 MAR 1999; 98WOJP00078.
FE	
XX	03 MAR 1999; 97US-004078C.
DK	(EISA) EISAI CO LTD.
VN	
XX	Kalyanaraman R., Kawai T., Zhu H.
Pt	WPf: 1998-495843/AZ.
LGR	
XX	Fibroblast growth factor mutcin and DNA having reduced receptor
Pt	binding and able to bind heparin, useful for treating and regulating
PE	heparin related disorders e.g. thrombotics
PS	Disclosed under page 59-60; /Tpp; English.
XX	
OY	This is the amino acid sequence of fibroblast growth factor-9
OC	(Fgf-9); claimed DNA molecule of the invention encode fgp mutcin
OC	fod peptides (see AAM75711-20) that show reduced fgf receptor binding
OC	activity but which retain the ability to bind heparin. For Fgf-9,
OC	amino acid residues 186, 143 and 146 are preferably replaced by
OC	other amino acid residues, with an optional further replacement of
OC	The glu-147 residue. The mutation may be further mediated by
OC	replacement of the cys residues to reduce aggregation. The mutcin
OC	is obtained by site specific or site directed mutagenesis of fgp-9
OC	rna. Incorporation of the mutated dna into a vector and expression
OC	in host cells. The fgp mutcins are used to treat heparin-related
OC	disorders, such as excessive bleeding induced by hepatic,
OC	ophthalamic disorders and hepatitis associated thrombocytopenia and
OC	thrombotosis. They may also be used to drug design.
XX	
SQ	Sequence : 208 AA:
Omely Match:	69-88 Score 774-5; DB 19; Length 208;
Best Local Similarity :	70-88; Prod No.: 74;
Matched Tag Conserved :	24; Mismatch: 40; Indels : 9; Gaps :

[illegible]


```

Db 6 1qfssldp-----vpldpspl100rlqfpeklrqpse-ldlhlkkltrrlqytr 59
QY 70 1qfssldp-----vpldpspl100rlqfpeklrqpse-ldlhlkkltrrlqytr 102
Db 60 1qfssldp-----vpldpspl100rlqfpeklrqpse-ldlhlkkltrrlqytr 119
QY 133 11SEGCPRGPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 192
Db 120 11SEGCPRGPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 179
QY 193 RPYDPERVPELYKIDLMY 210
Db 180 rpydpskpsmsrdlity 197

RESULT 41
AAV54432
1D AAV54432 standard: Peptide: 198 AA
XX
AC AAV54432:
XX
Db 27 MAR 2000 (first entry)
XX
DE Rat truncated fibroblast growth factor (RbFGF) (p. 4)
XX
KM Fibroblast growth factor, rat; hepatocyte proliferation;
KM hepatotrophic; fibroblast; viral hepatitis; cirrhosis; acute hepatitis;
KM fibroblast; fibrolytic product.
XX
OS Ratius sp.
XX
PN 05590473-A.
XX
PD 07-DBP-1999.
XX
PE 03-00T-1997: 97US-0943015.
XX
PR 03-00T-1997: 97US-0943015.
XX
PA (AMCIC) AMGEN INC.
XX
PI Arabican A. 1996 N. Fujikawa M. Martin PH.
XX
WF1. 2000 065457/07
XX
PI Fibroblast growth factor family polypeptide which stimulates
PI proliferation and growth of hepatocytes is useful for treating hepatic
PI disorders.
XX
PS Claim 18: Columns 43-44: 33pp: English.
XX
CC This sequence represents a truncated rat fibroblast growth factor-15
CC (RbFGF) does not, where residues 1-9 of the full length rat RbFGF-15
CC (AAV54432) have been removed by proteolytic cleavage. RbFGF-15 has
CC hepatocyte proliferation and growth activity, and increases hepatic
CC production of triglycerides and serum proteins (e.g., albumin). RbFGF-15
CC nucleic acids and/or proteins may be used for stimulating the
CC proliferation and development of hepatocytes both in vitro and in vivo.
CC The isolated nucleic acid molecules may be used directly in cell or gene
CC therapy applications to treat or prevent liver disorders, including
CC hepatic cirrhosis, fulminant liver failure, damage caused by acute viral
CC hepatitis and toxic insults to the liver.
XX
SQ Sequence 198 AA:

Query Match: 61.9%; Score 691.5; DB 21; Length 198;
Best Local Similarity 64.6%; Prod. No. 6,090-66;
Matches 128; Conservative 27; Mismatches 96; Indels 7; Gaps 4;

QY 14 11MCGVNSHPI1PACAPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 72
Db 6 1qfssldp-----vpldpspl100rlqfpeklrqpse-ldlhlkkltrrlqytr 59

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QY 70 1qfssldp-----vpldpspl100rlqfpeklrqpse-ldlhlkkltrrlqytr 102
Db 60 1qfssldp-----vpldpspl100rlqfpeklrqpse-ldlhlkkltrrlqytr 119
QY 133 11SEGCPRGPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 192
Db 120 11SEGCPRGPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 179
QY 193 RPYDPERVPELYKIDLMY 210
Db 180 rpydpskpsmsrdlity 197

RESULT 42
AAK55503
1D AAK55503 standard: peptide: 142 AA
XX
AC AAK55503:
XX
Db 06 MAR 1995 (first entry)
XX
DE G11a activating factor (GAF) peptide.
XX
KM G11a activating factor; GAF; testing; detection; antibody; cancer;
KM gastroenteritis; platelet; hepatopathy; cirrhosis; antitumor agent.
XX
OS Homo sapiens.
XX
PN P0608546-A.
XX
PD 04-AUG-1994.
XX
PE 18-DBP-1994: 94EP-0120491.
XX
PR 22-DBP-1992: 92JP-0442100.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Kurokawa T, Kuroshima K, Toku G, Yoshitomi S.
XX
WF1. 1994 242006/40
XX
PI New g11a activating factor polypeptide and antibodies - for use
PI in detection, purification and treatment of diseases, e.g. as
PI antitumor or platelet increasing agents.
XX
PS Disclature Page 40-49: 80pp: English.
XX
CC The g11a activating factor (GAF) polypeptides (see AAK55503-74511) can
CC be used as platelet increasing agents, osteoporosis promoting
CC agents or for treating related nervous disorders or hepatopathy such
CC as hepatic cirrhosis. They can also be used to treat cancer when
CC used alongside an antitumor agent. Antibodies directed against the
CC GAF polypeptides can be used for detecting or determining a
CC polypeptide activity or a GAF polypeptide or for purifying a GAF
CC polypeptide. The antibodies, which also can also be used for the growth
CC activity of GAF, can be used as antitumor agents.
XX
SQ Sequence 142 AA:

Query Match: 61.1%; Score 684; DB 15; Length 142;
Best Local Similarity 85.9%; Prod. No. 3,70-65;
Matches 122; Conservative 13; Mismatches 7; Indels 0; Gaps 1;

QY 57 1AMHCH11RPPGPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 116
Db 1 1qfssldp-----vpldpspl100rlqfpeklrqpse-ldlhlkkltrrlqytr 59

```


QY	1	MARLAEVETIGI	VELDQWVSHLL	PRADREKPI	LEEPSAARSGV	--GGRADJ	57	
DB	1	MARLAEVETIGV	VELDQWVSHLL	PRADREKPI	LEEPSAARSGV	--GGRADJ	54	
QY	1	MARLAEVETIGI	VELDQWVSHLL	PRADREKPI	LEEPSAARSGV	--GGRADJ	57	
DB	1	MARLAEVETIGV	VELDQWVSHLL	PRADREKPI	LEEPSAARSGV	--GGRADJ	54	
QY	58	AAH	HEHETRRQJ	YQVOTGRH	QAT	PRQSVYQVGRHQHDSLEFQ	LEPISVAQVLSIPQVRSQJ	117
DB	55	DHLK	ETTRRRQJ	YQVOTGRH	QAT	PRQSVYQVGRHQHDSLEFQ	LEPISVAQVLSIPQVRSQJ	114
QY	118	YLGQMR	CHLVSSLEHETTR	FEFGTEHNN	NTYSN	LYKRBZGKREFAVAL	AKRGTRPD	177
DB	115	YLGQMR	CHLVSSLEHETTR	FEFGTEHNN	NTYSN	LYKRBZGKREFAVAL	AKRGTRPD	174
QY	178	GAAPSRRQJ	FEHETTR	FEFGTEHNN	NTYSN	LYKRBZGKREFAVAL	AKRGTRPD	208
DB	175	GAAPSRRQJ	FEHETTR	FEFGTEHNN	NTYSN	LYKRBZGKREFAVAL	AKRGTRPD	205

RESULT 6
JC5941
Fibroblast growth factor 16 - Homo
Sapiens (Homo sapiens) (man)
Chromosome 16-Jul-1999 sequence_revision 16-Jul-1999 #test_change 21-Jul-2000
C.Accession: JC5941
P.Miyajima, A. Kikuchi, M. Matsuda, F. S. Ikeda, H. Akita, T. Ito, Y. Yamamoto, N. Miyazaki
Biochem. Biophys. Res. Commun. 243, 148-152, 1998
Title: Structure and expression of a novel member, FGF-16, of the fibroblast growth factor
A.Reference number: JC5940; MIM# 601098;
A.Accession: JC5941
A.Status: Preliminary
A.Molecule type: DNA
A.Keyword: 1997-MYB
A.Cross-references: DBU:AB009491; NID:q2911169; PUBM:BBA44956.1; PUB:q2911170
C.Superfamily: Fibroblast growth factor

Query Matched	63.1%	Score	209.57	EP	2	Length	207
Best Local Similarity	63.2%	Prod	209.57				
Matches	14	Conservative	27	Mismatches	40	Indels	11
						Gaps	43

[illegible]

RESULT 7
 J05940
 fibroblast growth factor 16 - rat
 C:Species: *Rattus norvegicus* (Norway rat)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C:Accession: J05940
 R:MI3070; A:Kishida, M., Kunita, F.H., Hiroshige, H., Aizawa, K., Yamamoto, S., Mikami
 Biochem. Biophys. Res. Commun. 243, 148-152, 1998
 A:Title: Structure and expression of a novel member, FGF-16, of the fibroblast growth factor
 A:Reference number: J05940; MIMD:98136888
 A:Accession: J05940
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residue: 1997 NTP
 A:Cross-references: DBJ:AB002561; NID:42911149; PIRN:MAA2947.1; EID:42911150
 C:Superfamily: fibroblast growth factor

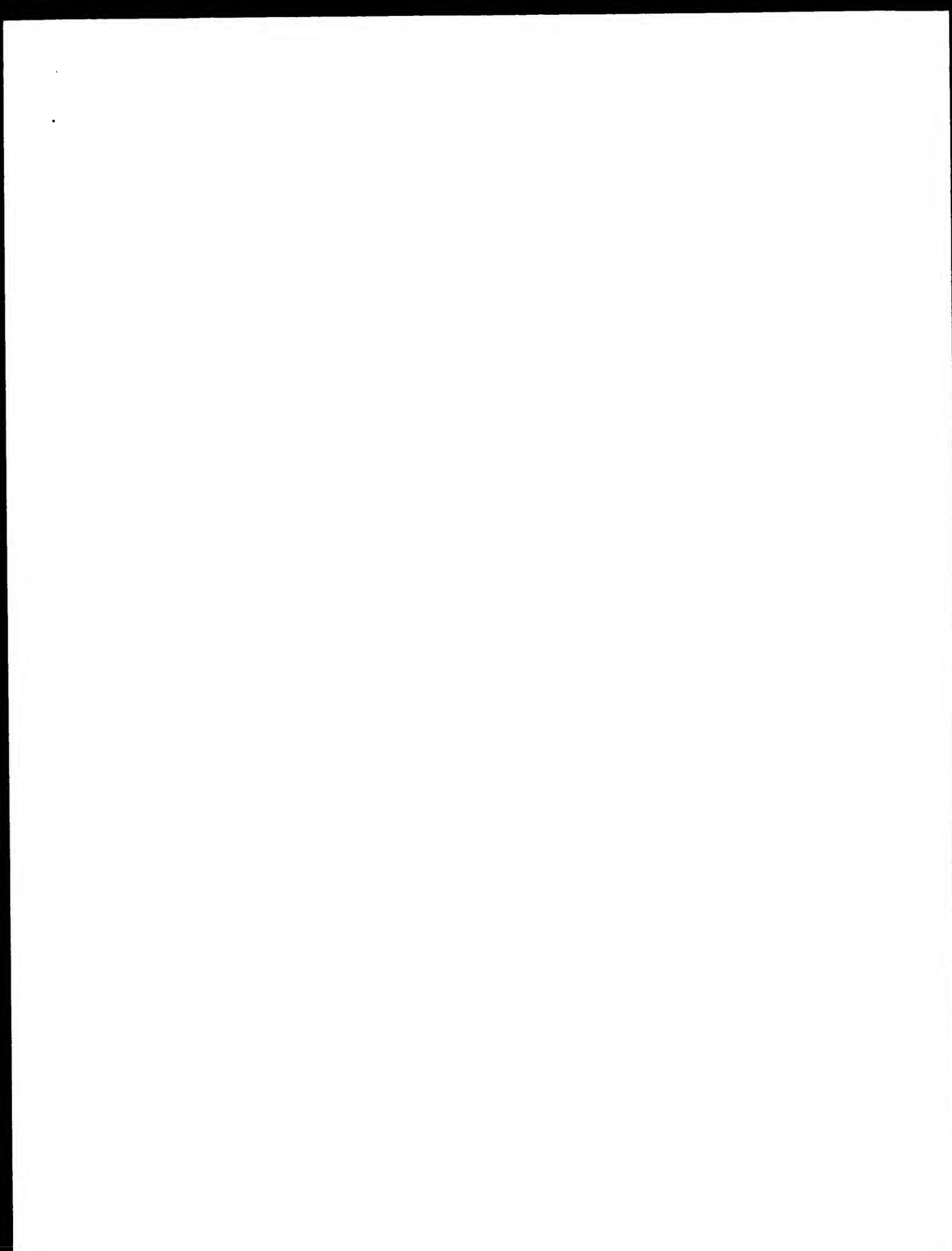
[illegible]

RESULT 8
 Legend
 1 Interblast growth factor 4 (chicken)
 2 Spectral Gattuso and Lee (chicken)
 3 Gattuso et al. Sep 1996. *Sequence_1 position 11 Sep 1996. *test_charac 17 Mar 2000
 4 Accession: 150588
 5 Mahmood, K., Kiefer, P., Guller, S., Dickson, C., Mason, L.
 Development 121, 1399-1410, 1996
 6 Title: Multiple roles for EGF signaling in early development. In: *Dev Biol*
 7 Reference number: 150588; MIMB:95469122
 8 Accession: 150588
 9 Status: preliminary; translated from (G/M/M/7/0/0)
 10 Molecule type: mRNA
 11 Position: 1-228 NMB
 12 Cross references: EMBL:U75557, GenBank:U75557, F00076A0374.5.11, F00076.2.216
 13 Species family: Interblast growth factor

[illegible]

CY 192 PRPW 196
11:1
DB 182 FKVL 186

RESULT 9
S68144
Fibroblast growth factor 5 - rat
Citation: FATHS, ROBERTSON, MURRAY, J.D.
Cloned: 06 Dec 1996 #sequence=1075101 Is Mar 1997 #text change 20 Jan 2000
Accession: S68144
Ratburly, Y., Yamashiki, M., Itoh, N.
Alcohol. Biophys. Acta 1386: 11-33, 1996
A.T.C.C. The 1st EFG 5 mRNA isolated from EFG 5
Accession number: S68144; MH0199201708
A:Accession: S68144
A>Status: preliminary; nucleic acid sequence not shown



FT	DOMAIN	53	59	POLY-SER.
FT	CATABOLISM	106	108	NET-LINKED (NUTRAC. & CATABOLISM)
FT	VARSPLIT	118	121	LEFT & RIGHT (IN SHORT ISOLFORM)
FT	VARSPIN	122	264	MISSING (IN SHORT ISOLFORM)
SQ	SYNTHESIS	264	264	FRANCOIS (ELEGANT) (ELEGANT)

Query Match	28.7%	Score 321	DB 1	Length 264
Best Local Similarity	40.3%	Prod. Nov. 9, 1923		
Matches	83	Conservative	22	Mismatches 75
			Indels	20
				2410
				7

QY	22	GSNHLIPACGRIP-----LJGDER-----KSAFAPSARGRIPAAUJALHJGIL-----	64
Db	22	QYVRLTEEDZAPYRHNSTQEDTEENALHSSASSSVAASTPVSQSGNDSHSTQWSP	81
QY	65	---PAPDLYPPT---GPHGDLIPGSEVQPTQOHSLFGLLEFTSVAGVLSIPGDSGLYL	119
Db	82	STGRLGSLYPPVRLTQPHQLTYPPQVNS--PQASTSLTFPAVYGLTGLTGVSENPPL	140
QY	120	THGQVLTTPQVPLTETPLSTTEENMYTVYVNLSTLHPLQVYVALRQDSTPLDPA	179
Db	141	AMSKVGLTQVASKATPLTQTFEPPECTYNLTVAGALHSTPLTETVNYVALNRYAVVQV	200
QY	180	---PSEBHQKTHPLPLIVLDFEVPPL	203
Db	201	SPVVKPQHVSTHPLTFRKQSDPL	225

RESULT	14
EGF3_HUMAN	
Id	EGF3_HUMAN
STANDARD:	
PRT	239 AA.

DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, last sequence update)
DT 15-JUL-1999 (Rel. 38, last annotation update)
DE INT 2. PROTONOMERON PROTEIN ENDOGENOUS (FIBROBLAST GROWTH FACTOR 3)

005 Homo sapiens (Human)
006 Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Mammalia; Euteleostomi;
007 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Hominidae; Homo;

RP SEQUENCING FROM N.A.
RC TISSUE: placenta;
XX MEDLINE-89239468; PubMed 2470097;

RI teratocarcinoma cells";
 RL oncogene 4:429-436(1989).
 CC -1- FUNCTION: COULD BE INVOLVED IN EAR DEVELOPMENT.

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cc or send an email to license@ibm-sib.ch.

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DR      HSSep: 009048; 2BEM.  
DR      MM: 164950; -  
DR      InterPro: IPR002299; Hsc70_EGF
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DR PRINTS: PRO0262; 111HRGF;
DR PRINTS: PRO0263; HBGFGEF;
DR P100nm: PD000831; HBSE_FGF; 1;
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	Transforming protein (Oncogene)	Growth factor	Mitogen	Signal
KW	Transforming protein (Oncogene)			
66	of protein.			
IT	SIGNAL	1	17	INITIATE
IT	CHAM	10	28	INT. & EXOGEN. GROW. FACTOR
IT	CHAM	45	65	RECEPTOR (GROWTH FACTOR)
50	SEQUENCE	219 AA	2686 AA	MOUSE 1702642606.8 (KCC4)

[illegible]

PB 17 PAAQPOCAL- HPIA-----MAGNY YHHEGTAOPPEKYNATYHLLHHS?VWAS 66

DD	S-LENSAVALIILIAVINGIVALIILIGIIGONYLAMKORIVAYASHYSALEIIVERTHEIA	125
67	S-LENSAVALIILIAVINGIVALIILIGIIGONYLAMKORIVAYASHYSALEIIVERTHEIA	125
09	148 YETIYANETI	197

QY 198 ERFPELYKII, 207

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RESULT 15
FCF3_MOUSE
T10_MOUSE
VARIABLE
PRT 1 2A5 A

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[illegible]

GN
FCF3 OR FCF4 OR IN1-2.
This material is (house).
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RN
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SCIENCE FROM N.A.
MEDLINE=86247592; PUBMED 4014624;
MEDLINE=86247592; PUBMED 4014624;

[illegible]

FA: Multiple POU domain proteins expressed in the embryonic midbrain and hindbrain. *Development* 124:1111-1120.

[illegible]

R1 CHAIRPERSON OF THE BOARD OF DIRECTORS
R1 FAMILY?
R1 F. J. CELL SOI. SQUAD. 13-87-96(1990).
CC PROSECUTION COUNCIL RE INVEYED IN PAR DEVENEMENT.

CC-1 SIMILARITY RELATES TO THE DECAPIN BINDING GROWIN FACTORS FAMILY.

CC-2

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CC-4 BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL COLLABORATION

RP SEGMENTE FROM N.A.
RC TISSUE lung
RA Jimenez P.A., Gubler J.R., Liu B., Feng P., Florence C., Blunt A.,
Haddad-Garcia K.A., Telsio M., Alluave F., Coleman T.A., Ortlitz D.M.,
Dillon P.A., Dunn R.D.
RT "Colaneous wound healing by normal growth factor 2" =
RC Submitted (7/11/99) to the *EMBO Molecular Biology* journal
RT -1- FUNCTION: COULD BE A GROWTH FACTOR ACTIVE IN THE PROCESS OF WOUND

RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN WISTAR,
 EX MELBINE 9627030; PubMed 962722;
 RA Yashiki M, Morita A, Takeda S, et al. 1997
 Structure and expression of the rat mRNAs encoding a novel member of

RL The fibroblast growth factor family."
 RL Biol. Chem. 271:15918-15921(1996).
 CC FUNCTION: COULD BE A GROWTH FACTOR ACTIVE IN THE PROCESS OF WOUND
 CC HEALING. ACTS AS A MITOGEN IN INT. JUNT. MAY ACT IN A MAJNER
 CC SIMILAR TO FGF-7.
 CC SUBCELLULAR LOCATION: SECRETED (POTENTIAL).
 CC TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE LONG IN
 CC ADULTS.
 CC SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
 CC
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 CC
 DR EMBL: D09217; K041166.1;
 DR InterPro: IPR002209; HGFP_FGF.
 DR InterPro: IPR002448; H1_HGFP.
 DR Pfam: PF00167; FGF_1.
 DR PRINTS: PR002442; H1HGFP.
 DR PRODOM: PD000841; HGFP_FGF_1.
 DR SMART: SM00442; FGF_1.
 DR PROSITE: PS00247; HGFP_FGF_1.
 DR Growth factor: glycoprotein signal.
 DR SIGNAL: 1 46 POTENTIAL.
 DR CHAIN: 47 215 FIBROBLAST GROWTH FACTOR-10.
 DR DOMAIN: 51 69 POLY-SER.
 DR CATHEDR: 50 50 N-LINKED (GLYCNA...) (POTENTIAL).
 DR CATHEDR: 204 204 N-LINKED (GLYCNA...) (POTENTIAL).
 DR SOURCE: 215 AA; 24029 MW; 94778FA6FC0866A CRC64;
 CC
 CC Query Match 27.5% Score 368, DB 1, Length 215,
 CC Best Local Similarity 36.4% Pred. No. 1, 1e-21;
 CC Matches 66, Conservative 47, Mismatches 67, Indels 10, Gaps 3.
 CC
 CC 19 GAVAGVAVSTGVYDSCGYLGNCKGPTVGSKRITSPQTFRQPEENMYNNYNNYKRGDI 161
 CC 47 GAVAGVAVSTGVYDSCGYLGNCKGPTVGSKRITSPQTFRQPEENMYNNYNNYKRGDI 93
 CC 74 GPHLGLTPGASVQGRKQDHSLEFLETSVAVGVVSLKGVLSDDIATMKNKDLVASENL 133
 CC 94 FTLEKTFPKKVSCTKFTFDPVETITTCVETVAVVAFVLSHYVYAMKKEKLYKSKKEI 159
 CC 144 TCEETLNGGTLAWTGVSSNIVYHSGFGRPVVALNKQTPQVAPSPHCKFTHEP 194
 CC 194 RRGVETKLELDRVRYVAVSWGH PREMYVAWLPVADPSELPKTSKPTSAHPL 211
 CC 194 PW 196
 CC 212 VV 214
 CC
 CC RESULT 20
 CC FROM HUMAN
 CC ID FGF1_HUMAN STANDARD: PRT: 170 AA.
 CC AC G9870;
 CC 20 AUG 2001 (rel. 40, last sequence update)
 CC 20 AUG 2001 (rel. 40, last annotation update)
 CC 20 AUG 2001 (rel. 40, last annotation update)
 CC FIBROBLAST GROWTH FACTOR-22 PRECURSOR (FGF-22).
 CC FGF22.
 CC Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 CC NCBI_TaxID:9606;
 CC 111
 CC SEQUENCE FROM N.A.
 CC RP
 CC TISSUE: Placenta;

RX MEDLINE:21240339; PubMed:11342227;
 RA Nakatani Y., Hoshikawa M., Asaki T., Kassai Y., Itoh N.,
 RT "Identification of a novel fibroblast growth factor, FGF 22,
 RT preferentially expressed in the inner root sheath of the hair
 RT follicle."
 RT Biochim. Biophys. Acta 1517:460-463(2001).
 CC -1- FUNCTION: MAY BE INVOLVED IN HAIR DEVELOPMENT.
 CC -1- SUBCELLULAR LOCATION: SECRETED (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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 CC
 DR EMBL: AB021925; BAB14479.1;
 DR MIM: 605831;
 DR InterPro: IPR002209; HGFP_FGF.
 DR InterPro: IPR002448; H1_HGFP.
 DR Pfam: PF00167; FGF_1.
 DR PRODOM: PD000841; HGFP_FGF_1.
 DR SMART: SM00442; FGF_1.
 DR PROSITE: PS00247; HGFP_FGF_1.
 DR Growth factor: signal.
 DR SIGNAL: 1 22 POTENTIAL.
 DR CHAIN: 23 170 FIBROBLAST GROWTH FACTOR-22.
 DR SOURCE: 170 AA; 19662 MW; C88891BC215AC67 CRC64;
 CC
 CC Query Match 27.5% Score 407; DB 1, Length 170,
 CC Best Local Similarity 45.0% Pred. No. 1, 1e-21;
 CC Matches 66, Conservative 23, Mismatches 56, Indels 4, Gaps 2;
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 CC 42 SAAPSPAPGPGGACGAIHNGHILPRQLYCGRGGHGLIPROSGVSTRODHSLEFLE 101
 CC 20 AATSPASAPGPP--PSYHLEFGVMPWPLESSSTHEPIVNDGAGVGTBRKBRHSDSLTE 77
 CC 102 SVAVGVAVSTGVYDSCGYLGNCKGPTVGSKRITSPQTFRQPEENMYNNYNNYKRGDI 161
 CC 78 SVAVGVAVSTGVYDSCGYLGNCKGPTVGSKRITSPQTFRQPEENMYNNYNNYKRGDI 145
 CC 162 GPEYVVALNKGITPRVAVSPHCKFTHEP 192
 CC 136 GQPMPLAIDPRGSPRPSGKTRVHLSAHLPL 166
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 CC RESULT 21
 CC FROM HUMAN
 CC ID FGF1_HUMAN STANDARD: PRT: 256 AA.
 CC AC P48802;
 CC 01-FEB-1996 (rel. 33, last sequence update)
 CC 01-FEB-1996 (rel. 33, last sequence update)
 CC 01-NOV-1997 (rel. 35, last annotation update)
 CC FIBROBLAST GROWTH FACTOR-3 PRECURSOR (FGF-3) (HGFP-3).
 CC FGF3 OR FGF-3.
 CC Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Danio; Zebrafish; Danio.
 CC Cypriniformes; Cyprinidae; Rasbora; Rasbora.
 CC NCBI_TaxID:7955;
 CC 111
 CC SEQUENCE FROM N.A.
 CC MEDLINE:96204005; PubMed:8622866;
 CC Kiefer P., Strahle U., Mason I., Dieckson C.,
 CC "Secretion and mitogenic activity of zebrafish FGF3 reveal
 CC intermediate properties relative to mouse and Xenopus homologues."
 CC Oncogene 12:1503-1511(1996).
 CC -1- FUNCTION: POTENT MITOGEN AND TRANSFORMING AGENT (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.


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980 Enkaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
981 Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Murinae; Mus-
982 Nchi_Taxid=10090;
983 RN [1]
984 RP SEQUENCE FROM N.A.
985 RX MEDLINE=97473538; PubMed=9332492;
986 PA Tqashira S., Harada H., Katsushita T., Itoh N., Nakatsuji M.:
987 "Cloning of mouse Fgf10 and up-regulation of its gene expression
988 during wound healing.";
989 RL Gene 197; 399-404(1997);
990 RN [2]
991 RP SEQUENCE FROM N.A.
992 RC TISSUE=Lung;
993 RA Duan B.R., Florence G.;
994 Submitted (MAR-1997) to the GenBank database.
995 CC FUNCTION: COULD BE A GROWTH FACTOR ACTIVE IN THE PROCESS OF WOUND
996 HEALING. ACTS AS A MITOGEN IN THE LUNG. MAY ACT IN A HARKER-
997 SIMILAR TO FGF-7.
998 CC -1- SINGLE CELL LOCATION: SECRETED (POTENTIAL).
999 CC -1- TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY IN EMBRYOS AND THE LUNG,
1000 AIR AT EACH LOWER LEVELS IN BRAIN AND HEART.
1001 CC -1- SIMILARITY: BELONGS TO THE HEPATIN BINDING GROWTH FACTORS FAMILY.
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1008 CC CC
1009 DR EMAIL: DB9080; BAA22838.1; ?
1010 DR EMAIL: U94517; AMPO0761.1; ?
1011 DR MGP: MG1:1099809; RGT10.
1012 DR InterPro: IPRO02209; HGCF_FGF.
1013 DR InterPro: IPRO02348; IL1_HBGF.
1014 DR Pfam: PF00167; FGF_1.
1015 DR PRINTS: PR00262; IL1HBGF.
1016 DR PRINTS: PR00263; HBGFEGF.
1017 DR TrEMBL: EF00831; HBGF_FGF_1.
1018 CR SMART: SMG0412; FGF_1
1019 DR PROSITE: PS00247; HBGF_FGF_1.
1020 KW Growth factor, glycoprotein; Signal.
1021 FT SIGNAL 1..36 POTENTIAL.
1022 FT CHAIN 37..209 FIBROBLAST GROWTH FACTOR-10.
1023 FT DOMAIN 52..63 POLY-SER.
1024 FT CARBOHYD 50..50 N-LINKED GLYCOP... (POTENTIAL).
1025 FT CARBOHYD 197..197 N-LINKED GLYCOP... (POTENTIAL).
1026 SO SEQUENCE 209 AA; 23597 MW; 7FD2E227H4F43CC CRCQ4;
1027
1028 SNOUTY Match 25.4%; Score 297; DP 1; Length 209;
1029 Best Local Similarity 40.9%; Pred. No. 1 20-20;
1030 Matches 54; ConservedAtts 32; Missed Atts 17; Indels 2; Claps 1;
1031
1032 YR HUMANKRKYAVKGIHQVLIIVASVGIIIGIDISLGVIAVAAGVSLIADVSGLY IIR
1033 II I I I I I I I I I I I I I I I I I I I I I I I I I I I I
1034 GA HQGVASWHLITFTLLIKKRVQLTKLVVLTCLVVLAIVLVGVAVAKLRDI... 172
1035
1036 QY LIY LGNNIKGLYSSEKIETSCIFREDFENMYNYSYNLYKHGDDEKRFVALNKRIIPRM 178
1037 II I I I I I I I I I I I I I I I I I I I I I I I I I I I I
1038 DB ILS LAHHKKRGKLYSKIEFNINIKLEPIELNGNYNSFWGG--NQGVYVALNRGAAPPG 190
1039 QY IYR ARSRHKQKETHPLRPV 195
1040 IIII :
1041 DB IYI GKTEPKNTSAHELPMT 207
1042 RESULT 25
1043 FGF7_CANFA
1044 ID FGF7_CANFA STANDARD PRT 194 AA.
1045 P79150;
1046 CT 20-AUG-2001 (Ref. 40, Cited)
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oc Xenoepidemic Xenoepid.
ox NRI TaxID 8456;
on 111
rp SOURCE FROM N.A.
rx MEDLINE: 9437010; PubMed 1013656;
ra Isaac H.V., Lamabelli D., Slack J.M.W.;
rt "Expression of a novel FGF in the Xenoepid embryo. A new candidate
rt inducing factor for mesoderm formation and anteroposterior
rt specification."
bl DEPOSITION: 114-711-720(1992).
cc 1 FUNCTION: GROWTH CANDIDATE FOR AN INDUCING FACTOR WITH POSSIBLE
cc ROLES BOTH IN MESODERM INDUCTION AT THE BLASTULA STAGE AND IN THE
cc INDUCTION OF THE ANTERIOPOSTERIOR AXIS AT THE GASTRULA STAGE.
cc 1 SUBCELLULAR LOCATION: SECRETED (PROBABLY).
cc 1 SIMILARITY: BELONGS TO THE HEPARIN BINDING GROWTH FACTORS FAMILY.
cc
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cc or send an email to license@isb.ch).
cc
cc EMBL: X62794; CAA4479.1;
cc DSSN: P09038; HGF.
cc InterPro: IP002209; HGCF_FGF.
cc LocPro: IP002348; 111_HGCF.
cc Pfam: PF00167; FGF_1.
cc PRINTS: PR00262; 11HGCF.
cc PRODOM: PD00831; HGCF_FGF_1.
cc PROSITE: PS00442; FGF_1.
cc SMART: SM00442; FGF_1.
cc PROSITE: PS00247; HGCF_FGF_1.
cc Growth factor; Mitogen; Signal.
cc KW SIGNAL.
cc FT CHAIN 23 187 FIBROBLAST GROWTH FACTOR-4-1.
cc SEQUENCE 187 AA: 21223 MW: 4465265820180 CRC64:

```

Query Match 25.0%; Score 279.5; DB 1; Length 187;
 Best Local Similarity 48.4%; Pred. No. 4.4e-19;
 Matches 62; Conservative 26; Mismatches 49; Indels 25; Gaps 5;

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oy 122 GILRRQLYCRGTFHLLDLPNGSVGCTRODHSIFGILFISVAVGLVSRGVNSGLYICM 121
db 62 GILRRQLYCRGTFHLLDLPNGSVGCTRODHSIFGILFISVAVGLVSRGVNSGLYICM 121
oy 122 NUGELGSEKLTSECTFPEPEENNYNNYNNYHGDGPRYFVALNKGDTPRKARS 181
db 122 NUGELGSEKLTSECTFPEPEENNYNNYNNYHGDGPRYFVALNKGDTPRKARS 181
oy 182 KRQKFTFLPRV 195
db 182 KRQKFTFLPRV 195
oy 180 KRQKFTFLPRV 193
db 180 KRQKFTFLPRV 193

```

RESULT 36
 FGF8_HUMAN STANDARD: PRT: 225 AA.
 AC Q92914;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, last sequence update)
 DT 01-NOV-1997 (Rel. 35, last annotation update)
 DE FIBROBLAST GROWTH FACTOR-11 (FGF-11) (FIBROBLAST GROWTH FACTOR
 DE HOMOLOGOUS FACTOR 3) (FHF-3).
 GN FGF11 OR FHF3.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID 9606;
 ON 111
 RP SOURCE FROM N.A.
 RC TISSUE-Relina;
 RX MEDLINE: 96382556; PubMed 8790420;
 RA Smallwood P.M., Munoz-Sanjuán I., Tong P., Macke J.P.,
 RA Hendry S.H., Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.;
 RT "Fibroblast growth factor (FGF) homologous factors: new members of

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oc TISSUE-Endometrium;
ra Ka H., Spencer T.E., Bazer F.W.;
rt "Keratinocyte growth factor: expression by endometrial epithelia of
rt the porcine uterus."
bl DEPOSITION: 114-711-720(1992).
cc 1 FUNCTION: GROWTH FACTOR ACTIVE ON KERATINOCYTES. POSSIBLE MAJOR
cc PARACRINE EFFECTOR OF NORMAL EPITHELIAL CELL PROLIFERATION (BY
cc SIMILARITY).
cc 1 SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
cc 1 SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
cc
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cc entities requires a license agreement (See: http://www.isb.ch/submit/submit.htm
cc or send an email to license@isb.ch).
cc
cc EMBL: AF217463; AAF26734.1;
cc InterPro: IP002209; HGCF_FGF.
cc LocPro: IP002348; 111_HGCF.
cc Pfam: PF00167; FGF_1.
cc PRINTS: PR00263; HGCF_FGF.
cc PRODOM: PD00831; HGCF_FGF_1.
cc PROSITE: PS00442; FGF_1.
cc SMART: SM00442; FGF_1.
cc PROSITE: PS00247; HGCF_FGF_1.
cc Growth factor; Mitogen; Signal.
cc KW SIGNAL.
cc FT CHAIN 32 194 KERATINOCYTE GROWTH FACTOR.
cc CARBOHYD 45 45 N-LINKED (GLCNAC... ) (POTENTIAL).
cc SEQUENCE 194 AA: 22463 MW: 84498545473180 CRC64:

```

Query Match 25.0%; Score 279; DB 1; Length 194;
 Best Local Similarity 42.5%; Pred. No. 5.1e-19;
 Matches 57; Conservative 30; Mismatches 45; Indels 2; Gaps 1;

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oy 62 GILRRQLYCRGTFHLLDLPNGSVGCTRODHSIFGILFISVAVGLVSRGVNSGLYICM 121
db 62 GILRRQLYCRGTFHLLDLPNGSVGCTRODHSIFGILFISVAVGLVSRGVNSGLYICM 121
oy 122 NUGELGSEKLTSECTFPEPEENNYNNYNNYHGDGPRYFVALNKGDTPRKARS 181
db 122 NUGELGSEKLTSECTFPEPEENNYNNYNNYHGDGPRYFVALNKGDTPRKARS 181
oy 182 KRQKFTFLPRV 195
db 182 KRQKFTFLPRV 195
oy 180 KRQKFTFLPRV 193
db 180 KRQKFTFLPRV 193

```

RESULT 36
 FGF8_HUMAN STANDARD: PRT: 225 AA.
 AC Q92914;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, last sequence update)
 DT 01-NOV-1997 (Rel. 35, last annotation update)
 DE FIBROBLAST GROWTH FACTOR-11 (FGF-11) (FIBROBLAST GROWTH FACTOR
 DE HOMOLOGOUS FACTOR 3) (FHF-3).
 GN FGF11 OR FHF3.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID 9606;
 ON 111
 RP SOURCE FROM N.A.
 RC TISSUE-Relina;
 RX MEDLINE: 96382556; PubMed 8790420;
 RA Smallwood P.M., Munoz-Sanjuán I., Tong P., Macke J.P.,
 RA Hendry S.H., Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.;
 RT "Fibroblast growth factor (FGF) homologous factors: new members of

DR InterPro: IPR002209; HGFP_FGF.
 DR Pfam: PF00167; FGF_1.
 DR Prodom: P0000841; HGFP_FGF_1.
 DR SMART: SM00442; FGF_1.
 DR PROSITE: PS00247; HGFP_FGF_1.
 KW Growth factor.
 SQ SEQUENCE: 225 AA; 25179 MW; 5134399561441 CP664;
 Query Match: 24.4%; Score 271.5; DB 1; Length 225;
 Best Local Similarity: 44.2%; Pred. No. 36-18;
 Matches: 68; Conservative: 40; Mismatches: 74; Indels: 27; Gaps: 4;
 QY 29 PATERP-----LIGKRSAAERSARGGAAALAHGILRRK 67
 ID 18 EGRSPVSAQRVTPCKSLQKGLILLSKVKLQDPTKQKQKPE POLKQIVRK 74
 QY 68 QLYTPRHHLQIPKSSQGTQDHSILGLEFISVAVGLVSTKGVDSGLYAMNDKGL 127
 ID 75 LKRGQIVYLVANRSGSLGTHEDPSLHFNILVTLKVVTLGSAKTHYAMNAKSL 133
 QY 128 YGSRKLTGHTTHGQDILDMWTFYSSNYKGLTCHRYEVALNELTFEPAKSKKDKF 187
 ID 144 YSGHETLAWLELTVLHVVLAVALYEECEHAWTGLIKEDYMKCHIVKPKAA 193
 QY 188 HPLRK -YVDKRVELY 204
 ID 194 AHVPLKLVAVYKPSIL 212
 RESULT 49
 EGF4 HUMAN STANDARD: PRT: 206 AA.
 ID P08620;
 DT 01 AUG 1988 (Rel. 08, Created)
 DT 01 AUG 1988 (Rel. 08, Last sequence update)
 DT 20 AUG 2001 (Rel. 40, Last annotation update)
 DE FIBROBLAST GROWTH FACTOR 4 PRECURSOR (FGF-4) (HEPARIN SECRETORY
 TRANSFORMING PROTEIN) (HST-1) (HST) (TRANSFORMING PROTEIN KS3) (HBGF-
 4)
 OS Homo sapiens (human).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OS Mammalia; Eutheria; Primates; Catartida; Homiidae; Homo.
 OX NCBI_TaxID 9606;
 RN 111
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 88041096; PubMed 2959959;
 RA Yoshida T., Miyagawa K., Odagiri H., Sakamoto H., Little P.F.K.,
 RT Torada M., Sugimura T.;
 RT "Genomic sequence of hst, a transforming gene encoding a protein
 homologous to fibroblast growth factors and the int-2-encoded
 protein.";
 RT Proc. Natl. Acad. Sci. U.S.A. 84:7405-7409(1987).
 RN 121
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 87204291; PubMed 2953041;
 RA Taira M., Yoshida T., Miyagawa K., Sakamoto H., Torada M.,
 RA Sugimura T.;
 RT "cDNA sequence of human transforming gene hst and identification of
 the coding sequence regulated for transforming activity.";
 RT Proc. Natl. Acad. Sci. U.S.A. 84:2980-2984(1987).
 RN 131
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 8701716; PubMed 2957062;
 RA Belli I., Cortada A.M., Korn F.G., Greco A., Itmann M.,
 RA Hostillo C.;
 RT "An oncogene isolated by transfection of Kaposi's sarcoma DNA encodes
 a growth factor that is a member of the FGF family.";
 RT Cell 50:279-287(1987).
 RT FUNCTION: CAN TRANSFORM NIH 3T3 CELLS FROM A HUMAN STOMACH TUMOR
 (HSD) AND FROM KAPOSI'S SARCOMA (KS3). IT HAS A MITOGENIC
 ACTIVITY.

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 DR EMBL: J02986; AAB59555.1;
 DR EMBL: M17446; AAB59473.1;
 DR PIR: A28417; TVHUS.
 DR HSSP: P09038; HRF.
 DR MIM: 164980; HRF.
 DR InterPro: IPR002209; HGFP_FGF.
 DR InterPro: IPR002348; IL1_HGFP.
 DR Pfam: PF00167; FGF_1.
 DR PRINTS: PR00262; IL1HGFP.
 DR PRINTS: PR00263; HBGF_FGF.
 DR Prodom: P0000841; HGFP_FGF_1.
 DR SMART: SM00442; FGF_1.
 DR PROSITE: PS00247; HGFP_FGF_1.
 DR TRANSFORMING PROTEIN; Oncogene; Growth factor; Mitogen; Signal.
 KW TRANSFORMING PROTEIN; POTENTIAL.
 FT SIGNAL 1 27
 FT CHAIN 1 206
 FT SEQUENCE 206 AA; 22047 MW; 57EDCA0972A1569 CP664;
 Query Match: 24.2%; Score 270; DB 1; Length 206;
 Best Local Similarity: 41.7%; Pred. No. 3-86-18;
 Matches: 68; Conservative: 20; Mismatches: 59; Indels: 16; Gaps: 5;
 QY 33 RPLLEERSAERSARGGAAALAHGILRRRLCYKT--GRILOIIPKSSVQSTRO 90
 ID 57 RLPLVAPKFAAVSGAGD-----YLALIKELRIYCNWVIGPI QALPDRIGGAA 109
 QY 91 DSHLHGLLESAVAVGIVSLPYNISLIQMGKCKDYGCEKLTSPTEICEENNYNT 150
 ID 110 D-TRDSLELSPVERGVSTFGVASRFPVAMSSKGLYGSPPETDTEKRIILPNNYNA 168
 QY 151 YSSNIYKHGIDGRFVALNKKDPTPDGANSKRRHOKTHLPR 193
 ID 169 YRS-YKYPG---MFLALSKNKTKKGNVSTPMKVTPLPR 205
 RESULT 40
 EGF4_BOVIN
 ID P48803;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE FIBROBLAST GROWTH FACTOR-4 PRECURSOR (FGF-4) (HEPARIN SECRETORY
 TRANSFORMING PROTEIN) (HST) (HBGF-4).
 OS Bos taurus (bovine).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OS Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OS Bovidae; Bovinae; Bos.
 OX NCBI_TaxID: 9913;
 RN 111
 RP SEQUENCE FROM N.A.
 RP TISSUE: thymus;
 RX MEDLINE: 96032369; PubMed-7557455;
 RA Yu J.-C., Deschamps A.J., Wang L.M., Fleming T.P., Chedid M.,
 RA Miki T., Heidaran M.A.;
 RT "An unexpected transforming gene in calf-thymus carrier DNA: bovine
 hst.";
 RT Gene 162:333-334(1995).
 CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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KC Canine hearts.
 RL F07.7. Biochem. 181:67-73(1989).
 CC -1- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANTI-GENIC AGENTS
 CC IN VIVO AND ARE PUTTING MITOGENS FOR A VARIETY OF CELL TYPES IN
 CC VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND
 CC CONCENTRATION OF THESE 2 GROWTH FACTORS.
 CC -1- SUBUNIT: MONOMER.
 CC -1- MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN, ALTHOUGH LESS STRONGLY
 CC THAN DOES BFGF.
 CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY
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 CC
 CC EMBL: X60317; GAA2869.1;
 DR PIR: S0354; S0354.
 DR HSSP: P05230; ZAXM.
 DR InterPro: IPR002209; HGCF_FGF.
 DR Pfam: PF00167; FGF_1.
 DR ProDom: PD000831; HGCF_FGF_1.
 DR SMART: SM00442; FGF_1.
 DR PROSITE: PS00247; HGCF_FGF_1.
 KM Growth factor; Mitogen; Vascularization; Heparin-binding.
 KA PROPEP 1 15
 FT CHAIN 16 2152 HEPARIN-BINDING GROWTH FACTOR 1.
 FT CHAIN 22 2152 ENDOTHELIAL CELL GROWTH FACTOR ALPHA.
 FT BINDING 24 28 HEPARIN (HECTETAL).
 FT BINDING 113 116 HEPARIN (POTETAL).
 FT CONFLICT 31 32 2 2 (IN REF. 2).
 FT CONFLICT 39 39 R -> Y (IN REF. 2).
 FT R-ENTER 152 152
 SV SEQUENCE 152 AA; 17103 MW; ADE540A92FVABF4 CMC64;
 Query Match 22.8%; Score 254.5; DB 1; Length 155;
 Best local similarity 36.6%; Pred. No. 6; Seq. 17;
 Matches 63; Conservation 20; Missed Obs. 4; Indels 36; Gaps 4;
 QY 25 PIPAGEPPPIGEPSSAEPSSAAGGGAQIAHLLIPGQYCRGPHLQTHNG 83
 DB 16 ENLPHGNKKPKP-----LYOSMOCHPLRLNG 44
 QY 94 SVGGPDPGHSIPPIPIISAVAVIVSTPVSQELTIQNRKCHVSSKPTICDITNP 112
 DB 45 TVMTKDRSDHDIQIQAISVSGVYIKSTPGQYIAMQTSIIVSQSPSECELELPL 104
 QY 144 FNNWYGVGVYHCTGFEIVALLRGTFPEZAFQFUDKPTHTTPPV 175
 DB 105 EHNHYNTISK KHAF KNNFVN KKNNS KPNLPTNYGCAILLPLPV 152
 RESULT 45
 FQFL_MOUSE STANDARD: PRT: 155 AA.
 AC P10935;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-INT-1989 (Rel. 11, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE HEPARIN-BINDING GROWTH FACTOR 1 (PPIPSGQ (HGCF-1) (ACTIVE FIBROBLAST
 DE GROWTH FACTOR) (AFGF).
 GN FQFL OR FGF-1 OR FGFA.
 OS Mus musculus (Mouse); and
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090, 10116;
 RN 11
 RP SEQUENCE FROM N.A.

KC SPECIES Rat;
 KX MEDLINE 8924061; PubMed-2479029;
 EA South J. Sci. Yon G. C. G. Balchout F. K. Munson P. E. C.
 ET "The nucleotide sequence of rat heparin binding growth factor 1
 RT (HGCF-1)".
 RL Nucleic Acids Res. 17:2867-2867(1989).
 RN 12
 KC SEQUENCE FROM N.A.
 KC SPECIES MOUSE;
 KX MEDLINE 9020167; PubMed-2418443;
 RA Robert J. M., Basilio C., Goldfarb M., Hanb O., Martin G. R.;
 RT "Isolation of cDNAs encoding four mouse FGF family members and
 RT characterization of their expression patterns during embryogenesis".
 RL Dev. Biol. 146:451-464(1990).
 RN 13
 KC SEQUENCE FROM N.A.
 KC SPECIES H. GEF;
 KX MEDLINE 97129412; PubMed-8972905;
 RA Medial F., Harkshaw K.V., Chiu J.M.;
 RT "Cloning and characterization of the mouse Fgf 1 gene".
 RL Gene 179:231-236(1996).
 RN 14
 KC SEQUENCE FROM N.A.
 KC SPECIES MOUSE; SHALIN BALP/97;
 KX MEDLINE 97994746; PubMed-899980;
 RA Adam K.Y., Frostholm A., Harkshaw K.V., Evans J.E., Rother A.,
 RA Chiu J.M.;
 RT "Characterization of the 1b promoter of fibroblast growth factor 1
 RT and its expression in the adult and developing mouse brain".
 RL J. Biol. Chem. 271:30263-30271(1996).
 CC 1- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANTI-GENIC AGENTS
 CC IN VIVO AND ARE PUTTING MITOGENS FOR A VARIETY OF CELL TYPES IN
 CC VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND
 CC CONCENTRATION OF THESE 2 GROWTH FACTORS.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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 CC EMBL: X14242; GAA22448.1;
 DR EMBL: M10641; AAA27618.1;
 DR EMBL: U64459; AAC52969.1;
 DR EMBL: U64457; AAC52969.1;
 DR EMBL: U64458; AAC52969.1;
 DR EMBL: U67610; AAC52907.1;
 DR EMBL: S04147; S04147.
 DR PIR: D37460; D37460.
 DR HSSP: P05239; ZAXM.
 DR GDB: M6195515; Fg11.
 DR InterPro: IPR002209; HGCF_FGF.
 DR InterPro: IPR02448; ILL_HGCF.
 DR Pfam: PF00167; FGF_1.
 DR PRINTS: PR00262; TLHGCF.
 DR PRODOM: PD000831; HGCF_FGF_1.
 DR SMART: SM00442; FGF_1.
 DR PROSITE: PS00247; HGCF_FGF_1.
 KW Growth factor; Mitogen; Vascularization; Heparin-binding.
 FT PROPEP 1 15
 FT CHAIN 16 155 HEPARIN-BINDING GROWTH FACTOR 1.
 FT BINDING 24 28 HEPARIN (HECTETAL).
 FT BINDING 113 116 HEPARIN (POTETAL).
 SV SEQUENCE 155 AA; 17418 MW; 888044F9H4A161 CMC64;
 Query Match 22.8%; Score 254.5; DB 1; Length 155;
 Best local similarity 43.5%; Pred. No. 7; Seq. 17;

RESULT 50
 FGF2_BOVIN
 ID FGF2_BOVIN STANDARD PET 155 AA.
 AC P03969;
 DT 23-OCT-1986 (rel. 02, Created)
 DT 23-OCT-1986 (rel. 02, Last sequence update)
 DT 01-FEB-1996 (rel. 35, Last annotation update)
 DE HEPARIN-BINDING GROWTH FACTOR-2 PROTEIN (HGF-2) (BASIC FIBROBLAST
 DE GROWTH FACTOR) (BFGF) (PROSTATROPIN) [CONTAINS: KIDNEY-DERIVED GROWTH
 DE FACTOR].
 GN FGF2 OR FGF-2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eularchia; Cetartiodactyla; Fumivallia; Pecora; Bovidae;
 OC Bovinae; Bovinae; Bos.
 OX NCBI_TaxID:9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:8676186; PubMed:242715;
 RA Abraham J.A., Merz J.A., Whang J.L., Tumolo A., Friedman J.,
 RA Hjertqvist K.A., Gospodarowicz D., Fiddes J.C.;
 RT "Nucleotide sequence of a bovine clone encoding the angiogenic
 RT protein, basic fibroblast growth factor";
 RL Science 233:545-548(1986);
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:87217066; PubMed:3472745;
 RA Abraham J.A., Whang J.L., Tumolo A., Merz J.A., Fiddes J.C.;
 RT "Human basic fibroblast growth factor: nucleotide sequence, genomic
 RT organization, and expression in mammalian cells";
 RL Cold Spring Harb. Symp. Quant. Biol. 51:657-668(1986);
 RN [3]
 RP SEQUENCE OF 10-155.
 RX MEDLINE:86016721; PubMed:3862109;
 RA Esch F., Baird A., Ling N., Orsini N., Hill F., Pandey R., Rappaport R.,
 RA Gospodarowicz D., Boehlen P., Guillemin R.;
 RT "Primary structure of bovine pituitary basic fibroblast growth factor
 RT (FGF) and comparison with the amino-terminal sequence of bovine brain
 RT acidic FGF";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:6507-6511(1985);
 RN [4]
 RP SEQUENCE OF 1-9.
 RX MEDLINE:86295747; PubMed:3741423;
 RA Ueno N., Baird A., Esch F., Ling N., Guillemin R.;
 RT "Isolation of an amino terminal extended form of basic fibroblast
 RT growth factor";
 RL Biochem. Biophys. Res. Commun. 138:590-592(1986);
 RN [5]
 RP SEQUENCE OF 25-41.
 RX MEDLINE:8695426; PubMed:4081126;
 RA Baird A., Esch F., Boehlen P., Ling N., Gospodarowicz D.;
 RT "Isolation and partial characterization of an endothelial cell growth
 RT factor from the bovine kidney: homology with basic fibroblast growth
 RT factor";
 RL Regul. Pept. 12:201-213(1985);
 RN [6]
 RP SEQUENCE OF 21-40.
 RX MEDLINE:87119165; PubMed:3809608;
 RA Ueno N., Baird A., Esch F., Shimazaki S., Ling N., Guillemin R.;
 RT "Purification and partial characterization of a mitogenic factor from
 RT bovine liver: structural homology with basic fibroblast growth
 RT factor";
 RL Regul. Pept. 16:135-145(1986);
 RN [7]
 RP X-BAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RX MEDLINE:91095963; PubMed:1702556;
 RA Hsu H.T., Kamiya H., Chirino A., Faham S., Fox G.M., Arakawa T.;
 RT "Three-dimensional structures of acidic and basic fibroblast growth
 RT factors";
 RL Science 251:90-93(1991).

CC 1- FUNCTION. THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS
 CC IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES IN
 CC VITRO. THERE ARE DIFFERENCES IN THE HEPARIN BINDING SITE AND
 CC CONCENTRATION OF THESE 2 GROWTH FACTORS.
 CC 1- MISCELLANEOUS. THIS PROTEIN BINDS HEPARIN MORE STERICALLY THAN DOES
 CC AFGF.
 CC 1- STRUCTURE. SEE ALSO THE HEPARIN BINDING OF WITH FACTOR 2.
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 CC EMBL: M3440; AAA40518.1;
 CC PIR: A24664; CPROB.
 CC PIR: A24819; A24819.
 CC PIR: A24878; A24878.
 CC PDB: 1BAS; 31-OCT-93.
 CC InterPro: IPR022099; HGF_FGF.
 CC InterPro: IPR023489; IL1_HGF.
 CC Pfam: PF00167; FGF_1.
 CC PRINTS: PR02622; IL1HGF.
 CC PROSITE: PS00263; HGF_FGF.
 CC PROSITE: PS000841; HGF_FGF_1.
 CC SMART: SM00442; FGF_1.
 CC PROSITE: PS00247; HGF_FGF_1.
 CC Growth factor: Mitogenic; Vascularization; Hepato-binding;
 CC 3D-structure.
 CC PT PROPEP 1 9
 CC FT CHAIN 10 155
 CC FT SITE 25 40
 CC FT SITE 46 48
 CC FT SITE 88 90
 CC FT BINDING 27 41
 CC FT BINDING 116 119
 CC FT STRAND 40 44
 CC FT TURN 35 38
 CC FT TURN 39 43
 CC FT TURN 45 46
 CC FT STRAND 49 52
 CC FT TURN 55 56
 CC FT TURN 58 60
 CC FT STRAND 62 68
 CC FT TURN 69 70
 CC FT STRAND 71 76
 CC FT TURN 77 80
 CC FT STRAND 81 85
 CC FT TURN 87 94
 CC FT STRAND 91 94
 CC FT HELIX 95 101
 CC FT STRAND 103 107
 CC FT TURN 109 110
 CC FT STRAND 113 117
 CC FT TURN 121 122
 CC FT STRAND 124 124
 CC FT STRAND 127 127
 CC FT TURN 129 140
 CC FT STRAND 133 143
 CC FT STRAND 136 148
 CC FT TURN 141 142
 CC FT HELIX 144 146
 CC FT STRAND 148 151
 CC SEQUENCE 155 AA, 17250 MW, 3963737.07 Da, 0.7641

Query Match 18.7% Score 2099 1081 Length 155;
 Host Local Similarity 47.5% Pred. No. 1,4012;
 Matches 54; Conservative 20; Mismatches 60; InDels 10; Gaps 4;


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QY 1 MAPLAVGSGFGLAEGAGGVGSHFLTPVAGKRPVTLGFRKSAERSAAGCGAAGLAHL 60
DB 1 MAPLTVGAVGAGLGGAGGVGSHFLTPVAGKRPVTLGFRKSAERSAAGCGAAGLAHL 60
QY 61 HCHLRKQVYKRGPHQVLPKQVSGVGTRODHSLEFLETSVAVGLVSLKRVDSGLYLG 120
DB 61 HCHLRKQVYKRGPHQVLPKQVSGVGTRODHSLEFLETSVAVGLVSLKRVDSGLYLG 120
QY 121 MNRKGLVSEKLESETRFPGFELNMYVTSNITRKRGVGRVVALNKRGTPEOGAR 180
DB 121 MNRKGLVSEKLESETRFPGFELNMYVTSNITRKRGVGRVVALNKRGTPEOGAR 180
QY 181 SKRHKFTFPLDPRVPEVPELYKRLIMYT 211
DB 181 SKRHKFTFPLDPRVPEVPELYKRLIMYT 211

RESULT 2
QY09K05 PRELIMINARY: PRT: 212 AA.
ID QY09K05
AC 01-MAR-2001 (TREMblrel, 16, Created)
DB 01-MAR-2001 (TREMblrel, 16, last sequence update)
DT 01-JUN-2001 (TREMblrel, 17, last annotation update)
DE FIBROBLAST GROWTH FACTOR 20.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NX MGI_TaxID:10090.
KN 111
RP SEQUENCE FROM N.A.
RA 110b N.
RT "Mus musculus mRNA for FGF 20(FGF20).":
RE Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DB EMBL: AB049218; BAB16406.1;
DB MGI: MGI:189146; Fgf20.
DB InterPro: IPR002209; HGFP_FGF.
DB InterPro: IPR002348; IL1_HGFP.
DB Pfam: PF00167; FGF_1.
DB PRINTS: PR00262; IL1HGFP.
DB PRODOM: P000831; HGFP_FGF_1.
DB SMART: SM00442; FGF_1.
DB PROSITE: PS00247; HGFP_FGF_1.
SQ SEQUENCE: 212 AA; 24659 MW; 17ADHCEB915669EP CRC64.

Query Match 95.6%; Score 1069; DB 11; Length 212;
Best Local Similarity 94.8%; Pred. No. 6,50-93;
Matches 200; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAPLAVGSGFGLAEGAGGVGSHFLTPVAGKRPVTLGFRKSAERSAAGCGAAGLAHL 60
DB 1 MAPLTVGAVGAGLGGAGGVGSHFLTPVAGKRPVTLGFRKSAERSAAGCGAAGLAHL 60
QY 61 HCHLRKQVYKRGPHQVLPKQVSGVGTRODHSLEFLETSVAVGLVSLKRVDSGLYLG 120
DB 61 HCHLRKQVYKRGPHQVLPKQVSGVGTRODHSLEFLETSVAVGLVSLKRVDSGLYLG 120
QY 121 MNRKGLVSEKLESETRFPGFELNMYVTSNITRKRGVGRVVALNKRGTPEOGAR 180
DB 121 MNRKGLVSEKLESETRFPGFELNMYVTSNITRKRGVGRVVALNKRGTPEOGAR 180
QY 181 SKRHKFTFPLDPRVPEVPELYKRLIMYT 211
DB 181 SKRHKFTFPLDPRVPEVPELYKRLIMYT 211

RESULT 4
QY09K05 PRELIMINARY: PRT: 207 AA.
ID QY09K05
AC 01-MAR-2001 (TREMblrel, 16, Created)
DB 01-MAR-2001 (TREMblrel, 16, last sequence update)
DT 01-JUN-2001 (TREMblrel, 17, last annotation update)
DE FGF-16 PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NX MGI_TaxID:10090.
KN 111
RP SEQUENCE FROM N.A.
RA 110b N.
RT "Cloning and biological function of FGF-16 in the heart.":
RE Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DB EMBL: AF292504; AAC29501.1;
DB InterPro: IPR002209; HGFP_FGF.
DB InterPro: IPR002348; IL1_HGFP.
DB Pfam: PF00167; FGF_1.
DB PRINTS: PR00262; IL1HGFP.

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PT 01-MAY-2000 (TREMblrel, 13, last sequence update)
DT 01-JUN-2001 (TREMblrel, 17, last annotation update)
DB XPGF-20.
QY XPGF-20.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
NC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae.
OC Xenopodinae; Xenopus.
NX NCBI_TaxID:8355.
KN 111
RP SEQUENCE FROM N.A.
RA MEDLINE:94373151; PubMed:10441498.
FX Koda C., Adati N., Nakata K., Mikoshiba K., Furuhata Y., Sato S.,
KA Terada S., Sakai Y., Furukawa T., Sekizawa Y., Yoshizumi K.K.,
DE "Characterization of a novel member of the FGF family, XPGF-20, in
RT Xenopus laevis."
RL Biochem. Biophys. Res. Commun. 261:756-765(1999).
DB EMBL: AB012615; BAB3474.1;
DB HSSP: P05230; 2ABC.
DB InterPro: IPR002209; HGFP_FGF.
DB InterPro: IPR002348; IL1_HGFP.
DB Pfam: PF00167; FGF_1.
DB PRINTS: PR00262; IL1HGFP.
DB PRODOM: P000831; HGFP_FGF_1.
DB SMART: SM00442; FGF_1.
DB PROSITE: PS00247; HGFP_FGF_1.
SQ SEQUENCE: 208 AA; 23438 MW; 268881D36E757D4D CRC64.

Query Match 80.9%; Score 904.5; DB 13; Length 208;
Best Local Similarity 80.6%; Pred. No. 20-77;
Matches 170; Conservative 19; Mismatches 19; Indels 4; Gaps 2;

QY 1 MAPLAVGSGFGLAEGAGGVGSHFLTPVAGKRPVTLGFRKSAERSAAGCGAAGLAHL 60
DB 1 MAPLTVGAVGAGLGGAGGVGSHFLTPVAGKRPVTLGFRKSAERSAAGCGAAGLAHL 60
QY 61 HCHLRKQVYKRGPHQVLPKQVSGVGTRODHSLEFLETSVAVGLVSLKRVDSGLYLG 120
DB 61 HCHLRKQVYKRGPHQVLPKQVSGVGTRODHSLEFLETSVAVGLVSLKRVDSGLYLG 117
QY 121 MNRKGLVSEKLESETRFPGFELNMYVTSNITRKRGVGRVVALNKRGTPEOGAR 180
DB 121 MNRKGLVSEKLESETRFPGFELNMYVTSNITRKRGVGRVVALNKRGTPEOGAR 177
QY 181 SKRHKFTFPLDPRVPEVPELYKRLIMYT 211
DB 178 AKRHKFTFPLDPRVPEVPELYKRLIMYTS 208

RESULT 4
QY09K05 PRELIMINARY: PRT: 207 AA.
ID QY09K05
AC 01-MAR-2001 (TREMblrel, 16, Created)
DB 01-MAR-2001 (TREMblrel, 16, last sequence update)
DT 01-JUN-2001 (TREMblrel, 17, last annotation update)
DE FGF-16 PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NX MGI_TaxID:10090.
KN 111
RP SEQUENCE FROM N.A.
RA 110b N.
RT "Cloning and biological function of FGF-16 in the heart.":
RE Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DB EMBL: AF292504; AAC29501.1;
DB InterPro: IPR002209; HGFP_FGF.
DB InterPro: IPR002348; IL1_HGFP.
DB Pfam: PF00167; FGF_1.
DB PRINTS: PR00262; IL1HGFP.

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EN SEQUENCE FROM N.A.
 RP MEDLINE: 20112823; PubMed 10644710;
 RA Minor Subunit 1, Smallwood P.M., Nathans J.
 RT "Isoform diversity among fibroblast growth factor homologous factors
 is generated by alternative promoter usage and differential
 splicing."
 RL J. Biol. Chem. 275:2589-2597(2000).
 DR EMBL: AF199605; AAF41942.1;
 DR InterPro: IPR002209; HMG_FGF.
 DR InterPro: IPR002448; H1_HMG.
 DR Pfam: PF00167; FGF_1.
 DR PRINTS: PR00262; H1_HMG.
 DR PRODOM: P0000841; HMG_FGF_1.
 DR SMART: SM00442; FGF_1.
 DR PROSITE: PS00247; HMG_FGF_1.
 FT NTER 1
 SQ SQUENGE 257 AA; 26816 MW; P130767465480822 CIRC64;

Query Match 28.48; Score 416; DB 13; Length 237;
 Best Local Similarity 43.58; Pred. No. 6, to 22;
 Matches 64; Conservative 31; Mismatches 48; Indels 4; Gaps 2;

QY 60 LHGILRRGQYGRGHGHIIDIPDSVGGIKGHSILFGLLEISVAVGLVSLGVPSGLYL 119
 DB 57 LKGIATR-LGKQGYVLQMPHDSLDGKIDSSNSTLPLPLVGLRVVALGVGKGTGLYL 114
 QY 120 GHHGSLVATGSLKSLNLTLEGG ERMNRYSSSTTEGCTGEPYVALSPGCTTEKGA 179
 DB 115 ALNNHRELYLSLEDPENKSEVENYVYVSSMLYKQSGAMFLAKNEQVMKGN 174
 QY 180 KSKRDKETHTHPVDPPE--FVPLY 204
 DB 175 RVKRTKPAHREPRPLEVAMVERPSLH 201

RESULT 8
 ID 090906; PRELIMINARY; PRT; 252 AA.
 AN 090906;
 DT 01 NOV 1998 (TREMBLrel: 08, Created)
 DT 01 NOV 1998 (TREMBLrel: 08, Last sequence update)
 DT 01 JUN 2001 (TREMBLrel: 17, Last annotation update)
 DE FGF 4B.
 GN FGF14.
 OS Kattus novivoltus (Kati), and
 OS Mus musculus (Mouse).
 OR Fukuyama; Morad; Chordata; Craniata; Vertebrata; Euteleostomi;
 OR Mammalia; Eularchia; Rodentia; Sciurognathi; Muridae; Murinae; Kattus.
 OX NCBI_TaxID 10116; 10090;
 RN
 RP SEQUENCE FROM N.A.
 RT TISSUE BRAIN;
 RA MEDLINE 96267141; PubMed 9602045;
 RA Yamamoto S., Mikami T., Ohbayashi N., Ohta M., Itoh N.;
 RT "Structure and expression of a novel isoform of mouse FGF homologous
 RT factor (FHF)-4."
 RL Biochem. Biophys. Acta 1398:48-41(1998).
 DR EMBL: A6008908; AAA41544.1;
 DR EMBL: A6008907; AAA41544.1;
 DR HSSP: P03968; HMR.
 DR MGJ: MGJ109189; Fgf14.
 DR InterPro: IPR002209; HMG_FGF.
 DR Pfam: PF00167; FGF_1.
 DR PRODOM: P0000841; HMG_FGF_1.
 DR SMART: SM00442; FGF_1.
 DR PROSITE: PS00247; HMG_FGF_1.
 SQ SEQUENCE 252 AA; 26364 MW; 281781E6A63AB44 CIRC64;

Query Match 27.38; Score 412; DB 13; Length 252;
 Best Local Similarity 42.98; Pred. No. 1, to 21;

Matches 63; Conservative 41; Mismatches 49; Indels 4; Gaps 2;
 QY 60 LHGILRRGQYGRGHGHIIDIPDSVGGIKGHSILFGLLEISVAVGLVSLGVPSGLYL 119
 DB 73 LKGIATR-LGKQGYVLQMPHDSLDGKIDSSNSTLPLPLVGLRVVALGVGKGTGLYL 140
 QY 120 GHHGSLVATGSLKSLNLTLEGG ERMNRYSSSTTEGCTGEPYVALSPGCTTEKGA 179
 DB 131 AMNGEGLYPSLEPFPEKFKSEVENYVYVSSMLYKQSGAMFLAKNEQVMKGN 190
 QY 180 KSKRDKETHTHPVDPPE--FVPLY 204
 DB 191 RVKRTKPAHREPRPLEVAMVERPSLH 217

RESULT 9
 ID 042407; PRELIMINARY; PRT; 212 AA.
 AC 042407;
 DT 01 JAN 1998 (TREMBLrel: 05, Created)
 DT 01 JUN 1998 (TREMBLrel: 06, Last sequence update)
 DT 01 JUN 2001 (TREMBLrel: 17, Last annotation update)
 DE F1RPH1AST 6PWTB FACTOR 10
 OS Gallus gallus (Chicken).
 OR Fukuyama; Morad; Chordata; Craniata; Vertebrata; Euteleostomi;
 OR Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID 9031;
 RN
 RP SEQUENCE FROM N.A.
 RA MEDLINE 97330690; PubMed 9187149;
 RA Onouchi H., Nakagawa T., Yamamoto A., Araga A., Ohta T., Ishimaru Y.,
 RA Yoshida H., Kuwana T., Nishio T., Yamasaki M., Itoh N., Noji S.;
 RT "The mesenchymal factor, FGF10, initiates and maintains the outgrowth
 RT of the chick limb bud through interaction with FGF8, an apical
 RT ectodermal factor."
 RL Development 124:2235-2244(1997).
 DR EMBL: D86333; BAA24945.1;
 DR HSSP: P03968; HMR.
 DR InterPro: IPR002209; HMG_FGF.
 DR Pfam: PF00167; FGF_1.
 DR PRODOM: P0000841; HMG_FGF_1.
 DR SMART: SM00442; FGF_1.
 SQ SEQUENCE 212 AA; 23631 MW; A84C993272A0D90 CIRC64;

Query Match 27.28; Score 404.5; DB 13; Length 212;
 Best Local Similarity 37.28; Pred. No. 6, to 21;
 Matches 67; Conservative 35; Mismatches 67; Indels 11; Gaps 4;

QY 21 VSHRELLPACGERPLLEPPSAEERSAGGTGA-----GLAHHGILRRGQYGRGTP 75
 DB 37 LADMLSPATNS-----SSSSSSPSSPSSSAAGHVSYNHOGDVKRKKLYYKNI 92
 QY 76 HLOHLPDSVGGTRPDHSLFGLLEISVAVGLVSLGVPSGLYLGNQDGLYGSERLIS 145
 DB 93 FLKLEKNGVSGTKKKNCPISLLEITSVELGVAVKSLSNYLAAMKKKPVGSGEPNS 152
 QY 136 EELFRRPEENMYNYSNLYKKGIDGRYVALAKNDIPRGAARKKRKKTHPLPRV 195
 DB 153 DKLKLNILHSDNYVALAKMRK KQGMVALSKCATKRWGKTEPRH;ZMHPLDLY 210

RESULT 10
 ID 09GSX5; PRELIMINARY; PRT; 302 AA.
 AC 09GSX5;
 DT 01 JUN 2001 (TREMBLrel: 17, Created)
 DT 01 JUN 2001 (TREMBLrel: 17, Last sequence update)
 DT 01 JUN 2001 (TREMBLrel: 17, Last annotation update)
 DE FIBROBLAST GROWTH FACTOR 12 (FRAGMNT).
 GN FGF12.
 OS Mus musculus (Mouse).

DT 01-MAY-2000 (ITEMBLREL 13, last sequence update)
 DT 01-JUN-2001 (ITEMBLREL 17, last annotation update)
 DE FIBROBLAST GROWTH FACTOR 3 (FRAGMENT).
 GN FGF3.
 OS *Oryzias latipes* (Medaka fish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Atherinomorpha;
 OC Acanthomorphi; Acanthopterygii; Perciformes; Atherinomorpha;
 OC Belontiiformes; Adrianichthyidae; Oryziatidae; Oryziat.
 NCBI_TaxID=8090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN NHT.
 RX MEDLINE:20082974; PubMed:10613850;
 RA Ohshima M., Marino S., Yoda K., Wada H., Naruse K., Mitani H.,
 RA Shima A., Ozata K., Kimura M., Inoko H.
 RT Construction of a linkage map of the Medaka (*Oryzias latipes*) and
 RT mapping of the mutant locus defective in spontaneous patterning.
 RL Genome Res. 9:1277-1287(1999).
 DR FMBI: AH030463; BAA85129 1;
 DR HSSP: P03968; IBAK.
 DR InterPro: IPR002396; Pfam_PFT.
 DR InterPro: IPR002348; ILL_HBGF.
 DR Pfam: PF00167; FGF 1.
 DR PRINTS: PR00262; ILLHBGF.
 DR ProDom: PD000841; HBGF_FGF 1.
 DR SMART: SM00442; FGF 1.
 DR PROSITE: PS00247; HBGF_FGF 1.
 F1 NON_TER 1 1
 F1 NON_TER 87 87
 FT SEQUENCE 87 AA: 9985 MW: 1594366 P66H16956 CIRC64.
 SU SEQUENCE

Query Match: 11.0% Score 12.5; EB 13; Length 87;
 Best Local Similarity 44.1% Pval: No. 3.1e-05;
 Matches 29; Conservative 14; Mismatches 29; Indels 17; Gaps 1.

QY 122 REF:YVSVFLEEFLEFLILAMNYSLLH
 DB 1 NKGRIYASVINKRPFVPRFLEILYNYASVHSTFELDPDAGGSKRPATKRWVS 60
 QY 169 INKQIPVAVKSKRHKETFLPR 193
 DB 61 INKQIPVAVKSKRHKETFLPR 85

RESULT 49
 Q9PTV8 PRELIMINARY PRT 87 AA.
 AC Q9PTV8;
 DT 01-MAY-2000 (ITEMBLREL 13, created)
 DT 01-MAY-2000 (ITEMBLREL 13, last sequence update)
 DT 01-JUN-2001 (ITEMBLREL 17, last annotation update)
 DE FIBROBLAST GROWTH FACTOR 3 (FRAGMENT).
 GN FGF3.
 OS *Oryzias latipes* (Medaka fish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Atherinomorpha;
 OC Acanthomorphi; Acanthopterygii; Perciformes; Atherinomorpha;
 OC Belontiiformes; Adrianichthyidae; Oryziatidae; Oryziat.
 NCBI_TaxID=8090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN NHT.
 RX MEDLINE:20082974; PubMed:10613850;
 RA Ohshima M., Marino S., Yoda K., Wada H., Naruse K., Mitani H.,
 RA Shima A., Ozata K., Kimura M., Inoko H.
 RT Construction of a linkage map of the Medaka (*Oryzias latipes*) and
 RT mapping of the mutant locus defective in spontaneous patterning.
 RL Genome Res. 9:1277-1287(1999).
 DR FMBI: AH030463; BAA85130 1;
 DR HSSP: P03968; IBAK.
 DR InterPro: IPR002396; HBGF_FGF.

DR InterPro: IPR002348; ILL_HBGF.
 DR Pfam: PF00167; FGF 1.
 DR PRINTS: PR00262; ILLHBGF.
 DR ProDom: PD000841; HBGF_FGF 1.
 DR SMART: SM00442; FGF 1.
 DR PROSITE: PS00247; HBGF_FGF 1.
 F1 NON_TER 1 1
 F1 NON_TER 87 87
 FT SEQUENCE 87 AA: 9985 MW: 1594366 P66H16956 CIRC64.
 SU SEQUENCE

Query Match: 11.0% Score 12.5; EB 13; Length 87;
 Best Local Similarity 44.1% Pval: No. 3.1e-05;
 Matches 29; Conservative 14; Mismatches 29; Indels 17; Gaps 1.

QY 122 REF:YVSVFLEEFLEFLILAMNYSLLH
 DB 1 NKGRIYASVINKRPFVPRFLEILYNYASVHSTFELDPDAGGSKRPATKRWVS 60
 QY 169 INKQIPVAVKSKRHKETFLPR 193
 DB 61 INKQIPVAVKSKRHKETFLPR 85
 RESULT 50
 Q9NOV2 PRELIMINARY PRT 76 AA.
 AC Q9NOV2;
 DT 01-OCT-2000 (ITEMBLREL 15, created)
 DT 01-OCT-2000 (ITEMBLREL 15, last sequence update)
 DT 01-JUN-2001 (ITEMBLREL 17, last annotation update)
 DE BASIC FIBROBLAST GROWTH FACTOR (FRAGMENT).
 GN FGF2.
 OS *Oryzias latipes* (Medaka fish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Atherinomorpha;
 OC Acanthomorphi; Acanthopterygii; Perciformes; Atherinomorpha;
 OC Belontiiformes; Adrianichthyidae; Oryziatidae; Oryziat.
 NCBI_TaxID=8090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-FETAL PLACENTAL ARTERY;
 RA Zhang J., Tsai S.C., Naruse K.R.;
 RT Growth factor expression in ovine fetal placental artery endothelial
 RT cells.
 KL Submitted (RAE 2000) to the EMBL/GenBank/DDBJ databases.
 DR FMBI: AF250027; AAF65566 1;
 DR InterPro: IPR002209; HBGF_FGF.
 DR InterPro: IPR002348; ILL_HBGF.
 DR Pfam: PF00167; FGF 1.
 DR PRINTS: PR00262; ILLHBGF.
 DR ProDom: PD000841; HBGF_FGF 1.
 DR SMART: SM00442; FGF 1.
 DR PROSITE: PS00247; HBGF_FGF 1.
 F1 NON_TER 1 1
 F1 NON_TER 76 76
 FT SEQUENCE 76 AA: 9796 MW: 7598152 P09745 J820 CIRC64.
 SU SEQUENCE

Query Match: 11.0% Score 12.5; EB 6; Length 76;
 Best Local Similarity 49.0% Pval: No. 0.00021;
 Matches 25; Conservative 7; Mismatches 19; Indels 9; Gaps 0.

Search completed: April 11, 2002, 09:55:42
 Job time: 198 sec

Thu Apr 11 12:31:21 2002

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